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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>if Contact: Sheppard</u>	AA Sequence (#) _____	Dialog _____
Searcher Location: <u>tel: 308-4499</u>	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr. Link _____
Date Completed: <u>6/26/01</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2001, 10:47:39 : Search time 107.93 Seconds
(without alignments)
147.101 Million cell updates/sec

Title: US-09-615-872-1

Perfect score: 638

Sequence: 1 EVOLQSGALVKKPGASVKL.....YGNNGFTYWGCGTLVTVA 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mbc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-unclassified:*
13: SP-vertebrate:*
14: SP-virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	469.5	73.6	117	11	O9QXE9 mus musculu
2	466.5	73.1	117	11	O9QXFO mus musculu
3	444	69.6	109	11	O9J175 mus musculu
4	439	68.8	118	11	O9J1C4 mus musculu
5	426	66.8	114	11	O9J1B1 mus musculu
6	425	66.6	110	11	O9J177 mus musculu
7	423.5	66.4	117	11	O9J1C6 mus musculu
8	413.5	64.8	119	5	O9GYZ2 schistosoma
9	413	64.7	110	11	O9J1B3 mus musculu
10	412	64.6	124	4	O9UL92 homo sapien
11	399.5	62.6	125	4	O9UL95 homo sapien
12	397.5	62.3	119	4	O9UL94 homo sapien
13	379	59.4	116	4	O9UL89 homo sapien
14	362.5	56.8	109	11	O9J1B5 mus musculu
15	342.5	53.7	150	4	O9J298 homo sapien
16	340.5	53.4	157	4	O9J298 homo sapien
17	336	52.7	298	11	O9QYFO mus musculu
18	320.5	50.2	131	4	O9UL88 homo sapien
19	309	48.4	112	4	O9HCL1 homo sapien

20	307.5	48.2	116	4	O9UL93 homo sapien
21	305.5	47.9	113	4	O9UL90 homo sapien
22	302.5	47.4	121	4	O9UL71 homo sapien
23	299	46.9	122	4	O9UL84 homo sapien
24	298.5	46.8	119	4	O9UL73 homo sapien
25	294	46.1	118	4	O9UL72 homo sapien
26	293	45.9	118	4	O9UL91 homo sapien
27	290	45.5	437	11	O9J1A4 mus musculu
28	288.5	45.4	102	11	O9J179 mus musculu
29	289	45.3	147	4	O9Y509 homo sapien
30	288	45.1	124	6	O9N0W6 oryctolagus
31	286	44.8	124	6	O9N0W4 oryctolagus
32	275	43.1	150	4	O9S973 homo sapien
33	263.5	41.3	112	4	O9UGP3 homo sapien
34	255	40.0	95	4	O9ULB6 homo sapien
35	254.5	39.9	104	4	O9UL87 homo sapien
36	242	37.9	122	4	O9UL75 homo sapien
37	229.5	36.0	121	4	O9UL96 homo sapien
38	197.5	31.0	118	4	O9UL74 homo sapien
39	196	30.7	77	4	O75726 homo sapien
40	181.5	28.4	86	4	O75740 homo sapien
41	180	28.2	77	4	O75728 homo sapien
42	180	28.2	88	4	O75737 homo sapien
43	178	27.9	416	4	O9NPP6 homo sapien
44	177.5	27.8	82	4	O75729 homo sapien
45	170.5	26.7	77	4	O75741 homo sapien

ALIGNMENTS

RESULT	ID	Q9QXE9	PRELIMINARY:	PRT:	117 AA.
AC	O9QXE9;	01-MAY-2000 (TREMBlrel. 13, Created)			
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)				
DT	01-MAY-2000 (TREMBlrel. 16, Last annotation update)				
DT	01-MAR-2001 (TREMBlrel. 16, Last annotation update)				
DE	IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Clemens A., Rademakers A., Specht C., Koelsch E.;				
RL	Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.				
DR	EMBL; AJ225174; CAB65237.1; -				
DR	InterPro; IPR003006; -				
DR	InterPro; IPR003596; -				
DR	PIfam; PF00047; 1g; 1.				
DR	SMART; SM00406; IGV; 1.				
FT	NON_TER	117			
FT	NON_TER	1			
SO	SEQUENCE	117 AA; 13000 MW; CDDE2AF84D499734 CRC64;			
Query Match 73.6%; Score 469.5; DB 11; Length 117;					
Best Local Similarity 73.3%; Pred. No. 1.5e-42;					
Matches 88; Conservative 13; Mismatches 16; Indels 3; Gaps 1;					
OY	1	EVOLQSGALVKKPGASVLSKASGYFTNRFYWKVRPGGLEWIGELINPRGDDTF	60		
DB	1	EVOLQSGALVKKPGASVLSKASGYFTNRFYWKVRPGGLEWIGELINPRGDDTF	60		
OY	61	NEKFSRATLVFDKSSSTAYMOLSLTSDSAIYCTRSFYGNNTYGGGTGGLVTVA	120		
DB	61	NEKFSRATLVFDKSSSTAYMOLSLTSDSAIYCTRSFYGNNTYGGGTGGLVTVA	120		
RESULT	2	PRELIMINARY:	PRT:	117 AA.	
O9QXFO					

AC 090XFO;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
 DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Clemens A., Rademakers A., Specht C., Koelsch E.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ25171; CAB65236.1;
 DR InterPro: IPR003006;
 DR InterPro: IPR003596;
 DR Pfam: PF00047; 1g; 1.
 DR SMART: SM00406; 1g; 1.
 FT NON_TER 1
 FT NON_TER 117
 SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match 73.18; Score 466.5; DB 11; Length 117;
 Best Local Similarity 72.58; Pred. No. 3.1e-42;
 Matches 87; Conservative 15; Mismatches 15; Indels 3; Gaps 1;

OY 1 EVOLQSGAEIVKPGASVYKLSKASGYTFNFIYWKORPGGLEWIGENPRNGDTDF 60
 1 EVOLQSGPELVKPGASVYKSKASGYTFIDYKMKWKQSGKLEWIGDINPNNGSTY 60
 DB 1 NEKESRATLVTDKSSSTAYWQSLTSEDSAIYCTRSPYGNNGYGTWGGTLTVSA 120
 61 NEKESRATLVTDKSSSTAYWQSLTSEDSAIYCTRSPYGNNGYGTWGGTLTVSS 117
 61 NQKFKRATLVTDKSSSTAYWQSLTSEDSAIYCTRSPYGNNGYGTWGGTLTVSS 117

RESULT 3
 O9JL75 PRELIMINARY; PRT; 109 AA.
 ID O9JL75
 AC O9JL75;
 DT 01-OCT-2000 (TEMBLrel. 15, Created)
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
 DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-BALB/C;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
 acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF206031; AAF69329.1;
 DR InterPro: IPR003006;
 DR InterPro: IPR003596;
 DR Pfam: PF00047; 1g; 1.
 DR SMART: SM00406; 1g; 1.
 FT NON_TER 1
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 12118 MW; FF65E441B9F936A6 CRC64;

Query Match 69.64; Score 444; DB 11; Length 109;
 Best Local Similarity 74.88; Pred. No. 7.1e-40;
 Matches 83; Conservative 12; Mismatches 14; Indels 2; Gaps 1;

OY 10 ELVPGASVYKLSKASGYTFNFIYWKORPGGLEWIGENPRNGDTDFNEKESRAT 69
 1 ELVPGASVYKSKASGYTFNFIYWKORPGGLEWIGENPRNGDTDFNEKESRAT 60

OY 70 LTVDKSSSTAYWQSLTSEDSAIYCTRSPYGNNGYGTWGGTLTVSA 120
 61 LTVSKSSSTAYWQSLTSEDSAIYCTRSPYGNNGYGTWGGTLTVSS 109

RESULT 4
 O9ZIC4 PRELIMINARY; PRT; 118 AA.
 ID O9ZIC4
 AC O9ZIC4;
 DT 01-MAY-1999 (TEMBLrel. 10, Created)
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
 DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
 DE ANTI-PORCINE VCA-MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-BALB/C;
 RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
 RA Matis L.M., Evans M.J.;
 RT "Humanized porcine VCA-M-specific monoclonal antibodies with chimeric
 IgG2/G4 constant regions block human Leukocyte binding to porcine
 endothelial cells."
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 DOMAIN.
 DR EMBL: U78801; AAD00293.1;
 DR InterPro: IPR003006;
 DR InterPro: IPR003596;
 DR Pfam: PF00047; 1g; 1.
 DR SMART: SM00406; 1g; 1.
 FT NON_TER 1
 FT NON_TER 118
 SQ SEQUENCE 118 AA; 13036 MW; 90EEC559D31EC4FC CRC64;

Query Match 68.84; Score 439; DB 11; Length 118;
 Best Local Similarity 69.28; Pred. No. 2.7e-39;
 Matches 83; Conservative 13; Mismatches 22; Indels 2; Gaps 1;

OY 1 EVOLQSGAEIVKPGASVYKLSKASGYTFNFIYWKORPGGLEWIGENPRNGDTDF 60
 1 QVOVQSGAEIVKPGASVYKLSKASGYTFNFIYWKORPGGLEWIGAIYEDGDTY 60
 DB 1 NEKESRATLVTDKSSSTAYWQSLTSEDSAIYCTRSPYGNNGYGTWGGTLTVSA 120
 61 NEKESRATLVTDKSSSTAYWQSLTSEDSAIYCTRSPYGNNGYGTWGGTLTVSS 118
 61 TQKFRKATLVTDKSSSTAYWQSLTSEDSAIYCTRSPYGNNGYGTWGGTLTVSS 118

RESULT 5
 O9JL81 PRELIMINARY; PRT; 114 AA.
 ID O9JL81
 AC O9JL81;
 DT 01-OCT-2000 (TEMBLrel. 15, Created)
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
 DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-BALB/C;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
 acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF206025; AAF69323.1;
 DR InterPro: IPR003006;
 DR InterPro: IPR003596;


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RESULT 9
Q9UL83 PRELIMINARY; PRT; 110 AA.
AC Q9UL83;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206023; AAF69321.1;
DR InterPro; IPR003596;
DR Pfam; PF00047; 19; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT 110
SQ SEQUENCE 110 AA; 12052 MW; 84E6F2AD219AF95E CRC64;

Query Match 64.7%; Score 413; DB 11; Length 110;
Best Local Similarity 72.1%; Pred. No. 1,4e-36;
Matches 80; Conservative 12; Mismatches 17; Indels 2; Gaps 1;

QY 10 ELVPGASVYKLSKASGYTFNYFYWKORPGGLEWIGINRNDTPNEKESRAT 69
DB 2 ELVPGASVYKLSKASGYTFNSNMWVKLRPGGLEWIGITGYGDSGAYYNGFKKRA 61
QY 70 LTVDSSTAYVQLSLTSEDSATYCTSPYGNNGFTYWGQGLTVVSA 120
DB 62 LTVDSSTAYVQLSLTSEDSATYCTSPYGNNGFTYWGQGLTVVSA 110

RESULT 10
Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.;
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN
EMBL; AF035022; AAD56258.1;
DR InterPro; IPR003506;
DR Pfam; PF00047; 19; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT 124
SQ SEQUENCE 124 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

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SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match 64.6%; Score 412; DB 4; Length 124;
Best Local Similarity 62.1%; Pred. No. 2.1e-36;
Matches 77; Conservative 19; Mismatches 24; Indels 4; Gaps 1;

QY 1 EVOLQSGAEVLVPGASVYKLSKASGYTFNYFYWKORPGGLEWIGINRNDTPDF 60
DB 1 EVOLVESGAEVKKRPGASVYKLSKASGYTFSSYYMHVROAPGGGLEWIGINRSGSTSY 60
QY 61 NEKFEESATITLVKSSSTAYVQLSLTSEDSATYCTSPYGNNGFTYWGQGLTV 116
DB 61 AOKFGQGVMTTRDTSTYVMELSLSESDTAVAYCCARGLVYVPAFSPREDYWGQGLTV 120
QY 117 TVSS 120
DB 121 TVSS 124

RESULT 11
Q9UL95 PRELIMINARY; PRT; 125 AA.
AC Q9UL95;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.;
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN
EMBL; AF035019; AAD56255.1;
DR InterPro; IPR003506;
DR Pfam; PF00047; 19; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match 62.6%; Score 399.5; DB 4; Length 125;
Best Local Similarity 59.2%; Pred. No. 4.5e-35;
Matches 74; Conservative 21; Mismatches 25; Indels 5; Gaps 1;

QY 1 EVOLQSGAEVLVPGASVYKLSKASGYTFNYFYWKORPGGLEWIGINRNDTPDF 60
DB 1 EVOLVESGAEVKKRPGASVYKLSKASGYTFGYMHVROAPGGGLEWIGINRSGSTSY 60
QY 61 NEKFEESATITLVKSSSTAYVQLSLTSEDSATYCTSPYGNNGFTYWGQGLTV 115
DB 61 AOKFGQGVMTTRDTSTYVMELSLSESDTAVAYCCARSGGRIAAAGDAFIMGQGLTV 120
QY 116 TVSS 120
DB 121 TVSS 125

RESULT 12
Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;

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OM protein - protein search, using sw model

Run on: June 20, 2001, 11:13:49 ; Search time 33.18 Seconds

(Without alignments)
123.890 Million cell updates/sec

Title: US-09-615-872-1

Perfect score: 638
Sequence: 1 EVQLQSGAEIVKRGASVKL.....YGNNGFTYWGQGLTVASA 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 3425486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	485	76.0	139	1	P01751 mus musculu
2	480.5	75.3	138	1	P03980 mus musculu
3	475.5	74.5	140	1	P01746 mus musculu
4	474.5	74.4	120	1	P01747 mus musculu
5	457	71.6	137	1	P01755 mus musculu
6	454.5	71.2	117	1	P01757 mus musculu
7	452	70.8	120	1	P06329 mus musculu
8	448.5	70.3	117	1	P01756 mus musculu
9	437	68.5	118	1	P06330 mus musculu
10	433	67.9	117	1	P01748 mus musculu
11	431	67.6	117	1	P06328 mus musculu
12	427.5	67.0	121	1	P01745 mus musculu
13	422	66.1	117	1	P01750 mus musculu
14	422	66.1	117	1	P01753 mus musculu
15	418	65.5	117	1	P01754 mus musculu
16	412	64.6	117	1	P01749 mus musculu
17	400	62.7	117	1	P06327 mus musculu
18	396	62.1	117	1	P01758 mus musculu
19	394.5	61.8	136	1	P01759 mus musculu
20	374	58.6	147	1	P01744 homo sapien
21	361	56.6	117	1	P01743 homo sapien
22	355	55.6	117	1	P23083 homo sapien
23	351	55.0	114	1	P01741 mus musculu
24	337	52.8	119	1	P01807 mus musculu
25	334	52.4	119	1	P01801 mus musculu
26	330.5	51.8	115	1	P01812 mus musculu
27	326.5	51.2	117	1	P01812 mus musculu
28	326	51.1	122	1	P01768 homo sapien
29	323.5	50.7	115	1	P01802 mus musculu
30	322.5	50.5	113	1	P01800 mus musculu
31	322.5	50.5	142	1	P01805 rattus norv
32	321.5	50.4	113	1	P01796 mus musculu
33	321.5	50.4	113	1	P01799 mus musculu

34	320.5	50.2	117	1	HV1A_HUMAN	P01742 homo sapien
35	319	50.0	120	1	HV1H_HUMAN	P80421 homo sapien
36	317	49.7	119	1	HV38_MOUSE	P01808 mus musculu
37	316	49.5	124	1	HV1D_HUMAN	P01760 homo sapien
38	315.5	49.5	113	1	HV28_MOUSE	P01797 mus musculu
39	313.5	49.1	113	1	HV29_MOUSE	P01798 mus musculu
40	312.5	49.0	121	1	HV3J_HUMAN	P01771 homo sapien
41	310.5	48.7	125	1	HV1E_HUMAN	P06326 homo sapien
42	305.5	47.9	117	1	HV4I_MOUSE	P01811 mus musculu
43	302.5	47.4	118	1	HV39_MOUSE	P01809 mus musculu
44	298	46.7	116	1	HV3T_HUMAN	P01781 homo sapien
45	297	46.6	111	1	HV35_MOUSE	P01804 mus musculu

ALIGNMENTS

RESULT 1
ID HV07_MOUSE STANDARD: PRT: 139 AA.
AC P01751, P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION BI-8/186-2 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THE BI-8 MG CHAIN mRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----

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EMBL: J00529; AAA38170.1; -;
DR PIR: A02034; MHMS18.
DR InterPro: IPR003006; -;
DR Pfam: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION BI-8/186-2.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 76.0%; Score 485; DB 1; Length 139;
Best Local Similarity 76.0%; Pred. No. 1,1e-43;
Matches 92; Conservative 16; Mismatches 11; Indels 2; Gaps 2;

```

OY 1 EVOLQSGAELVPGASVKLSCKASGYTFNFIYWKQKPGGGLWIGINPRNDTDF 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 20 QVQLQPGALVPGASVKLSCKASGYTFNFIYWKQKPGGGLWIGINPRNDTDF 79
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 NEKFSRATLTVDKSSSTAVMQLSLTSEDSAIYYCTRSPYGNNGFTYWGGLTVTS 119
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 80 NEKFSKATLTVDKSSSTAVMQLSLTSEDSAIYYCARVDYGSY-FDYWGGLTVTS 138
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 120 A 120
DB 139 S 139

RESULT 2
HVA8_MOUSE
ID HV02_MOUSE STANDARD; PRT; 138 AA.
AC P01746;
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an IgD-secreting plasmacytoma."
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR: A02033; HYMS77.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 19; 1.
OY 1 Immunoglobulin V region; Signal.
DB 20 EVOLQSGAELVPGASVKLSCKASGYTFNFIYWKQKPGGGLWIGINPRNDTDF 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 NEKFSRATLTVDKSSSTAVMQLSLTSEDSAIYYCTRSPYGNNGFTYWGGLTVTS 119
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 80 NEKFSKATLTVDKSSSTAVMQLSLTSEDSAIYYCARVDYGSY-FDYWGGLTVTS 138
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 120 A 120
DB 139 S 139

RESULT 3
HVA8_MOUSE
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbits T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain."
RL Science 216:309-311(1982).
CC -----
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CC -----
DR EMBL: J00493; AAA38128.1; -.
DR PIR: A02028; HYMSG7.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 19; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 74.5%; Score 475.5; DB 1; Length 140;
Best Local Similarity 75.2%; Pred. No. 1e-42;
Matches 91; Conservative 13; Mismatches 16; Indels 1; Gaps 1;

OY 1 EVOLQSGAELVPGASVKLSCKASGYTFNFIYWKQKPGGGLWIGINPRNDTDF 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 20 EVOLQSGAELVPGASVKLSCKASGYTFNFIYWKQKPGGGLWIGINPRNDTDF 79
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 NEKFSRATLTVDKSSSTAVMQLSLTSEDSAIYYCTRSPYGNNGFTYWGGLTVTS 119
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 80 NEKFSKATLTVDKSSSTAVMQLSLTSEDSAIYYCARVDYGSY-FDYWGGLTVTS 139
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 120 A 120
DB 140 S 140

RESULT 4
HVA3_MOUSE
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=8331846; PubMed=6186498;
RA Stekevitz M., Gelfer M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idio type response of the strain A mouse."
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.

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DR PIR: A02028; HVM5G7.
 DR InterPro: IPR003006; -
 DR Pfam: PF00047; 19; 1.
 KM Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
 FT NON_TER 120 120
 SQ SEQUENCE 120 AA; 13307 MW; FF04EA167B654AF CRC64;

Query Match 74.4%; Score 474.5; DB 1; Length 120;
 Best Local Similarity 75.8%; Pred. No. 1,1e+42;
 Matches 91; Conservative 12; Mismatches 16; Indels 1; Gaps 1;

QY 2 VOLQSGAEIVKPPGASVYKLSCKASGYTFYFYVWKORPGGLEWIGETINPRNGDTDFN 61
 DB 1 VOLQSGAEIVKPPGASVYKLSCKASGYTFYFYVWKORPGGLEWIGETINPRNGDTDFN 60
 QY 62 EKESRATLTVDKSSSTAYMQLSLTSEDSATYYCTRSP-YGNNGYFTYWGQGLTVVSA 120
 DB 61 EKESRATLTVDKSSSTAYMQLSLTSEDSATYYCTRSP-YGNNGYFTYWGQGLTVVSS 120

RESULT 5
 HVL_MOUSE
 ID HVL_MOUSE STANDARD; PRT; 137 AA.
 AC P01755;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION S43 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81234548; PubMed=6788376;
 RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
 Baltimore D.;
 RT "Heavy chain variable region contribution to the NPB family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
 CC -1- MISCELLANEOUS: THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
 CC (NPB ANTIBODIES).
 CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
 CC (NPB ANTIBODIES).
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DR EMBL: J00539; AAA38172.1; -
 DR PIR: A02038; G2MS43.
 DR InterPro: IPR003006; -
 DR Pfam: PF00047; 19; 1.
 KM Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 137
 FT DOMAIN 20 49
 FT DOMAIN 50 54
 FT DOMAIN 55 68
 FT DOMAIN 69 85
 FT DOMAIN 86 117
 FT DOMAIN 118 122
 FT DOMAIN 123 137
 FT DISULFID 41 115
 FT NON_TER 137 137
 SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match

71.6%; Score 457; DB 1; Length 137;

Best Local Similarity 71.7%; Pred. No. 8.5e+41;
 Matches 86; Conservative 13; Mismatches 19; Indels 2; Gaps 1;

QY 1 EVOLQSGAEIVKPPGASVYKLSCKASGYTFYFYVWKORPGGLEWIGETINPRNGDTDF 60
 DB 20 EVOLQSGAEIVKPPGASVYKLSCKASGYTFYFYVWKORPGGLEWIGETINPRNGDTDF 79
 QY 61 NEKESRATLTVDKSSSTAYMQLSLTSEDSATYYCTRSP-YGNNGYFTYWGQGLTVVSA 120
 DB 80 NEKESRATLTVDKSSSTAYMQLSLTSEDSATYYCTRSP-YGNNGYFTYWGQGLTVVSS 137

RESULT 6
 HVL_MOUSE
 ID HVL_MOUSE STANDARD; PRT; 117 AA.
 AC P01757;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION J558.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=80078170; PubMed=6765983;
 RA Schilling J., Clevinger B., Davie J.M., Hood L.;
 RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
 RT rearrangements in heavy chain V-region gene segments.";
 RL Nature 283:35-40(1980).
 CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
 CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
 CC WHICH OCCUR IN THE D AND J SEGMENTS.
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
 DR PIR: A26242; MEMSJS.
 DR InterPro: IPR003006; -
 DR Pfam: PF00047; 19; 1.
 KM Immunoglobulin V region.
 FT DISULFID 22 96
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 71.2%; Score 454.5; DB 1; Length 117;
 Best Local Similarity 71.7%; Pred. No. 1.3e+40;
 Matches 86; Conservative 14; Mismatches 17; Indels 3; Gaps 1;

QY 1 EVOLQSGAEIVKPPGASVYKLSCKASGYTFYFYVWKORPGGLEWIGETINPRNGDTDF 60
 DB 1 EVOLQSGAEIVKPPGASVYKLSCKASGYTFYFYVWKORPGGLEWIGETINPRNGDTDF 60
 QY 61 NEKESRATLTVDKSSSTAYMQLSLTSEDSATYYCTRSP-YGNNGYFTYWGQGLTVVSA 120
 DB 61 NEKESRATLTVDKSSSTAYMQLSLTSEDSATYYCTRSP-YGNNGYFTYWGQGLTVVSS 117

RESULT 7
 HVS_MOUSE
 ID HVS_MOUSE STANDARD; PRT; 120 AA.
 AC P06329;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION AC38 15.3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=84182519; PubMed=6201362;
 RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;

Query Match	67.68;	Score 431;	DB 1;	Length 117;
Best Local Similarity	82.58;	Pred. NO. 3.6e-38;		
Matches 80; Conservative	11;	Mismatches 6;	Indels 0;	Gaps 0;

RESULT	13		
HY06_MOUSE			
ID	HY06_MOUSE	STANDARD:	PRT; 117 AA.
AC	P01750;		
DT	21-JUL-1986 (rel. 01, Created)		
DT	21-JUL-1986 (rel. 01, Last sequence update)		
DT	15-JUL-1999 (rel. 38, Last annotation update)		
DE	IG HEAVY CHAIN V REGION 102 PRECURSOR.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
NP	[1]		
	SEQUENCE FROM N.A.		

RC STRAIN-C57BL/6;
 RX MEDLINE-81234548; PubMed-6788376;
 RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
 RT "heavy chain variable region contribution to the NpB family of antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
 DR PIR: A02032; HVMS02.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; 1g; 1.
 KW Immunoglobulin V region; Signal.
 FT CHAIN 1 19
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DISULFID 86 117 FRAMEWORK 3.
 FT NON_TER 117 117 BY SIMILARITY.
 SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FC8C CRC64;

Query Match 66.1%; Score 422; DB 1; Length 117;
 Best Local Similarity 81.1%; Pred. No. 3.1e-37;
 Matches 77; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

QY 2 VOLOOSGAEELVKGASVSKSCASGYFTNYFYWVKORPGGLEWIGETINPRNGDTDF 61
 DB 21 VOLOOSGAEELVKGASVSKSCASGYFTNYFYWVKORPGGLEWIGETINPRNGDTDF 80
 QY 62 EKFESEATLVYDKSSSTAYWQLSLTSEDSAYVYC 96
 DB 81 EKFESEATLVYDKSSSTAYWQLSLTSEDSAYVYC 115

RESULT 14
 ID HV09_MOUSE STANDARD; PRT; 117 AA.
 AC P01753; P11271;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 IG HEAVY CHAIN V REGION 186-1 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6;
 RX MEDLINE-81234548; PubMed-6788376;
 RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
 RT "heavy chain variable region contribution to the NpB family of antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
 DR PIR: B02034; HVMS61.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; 1g; 1.
 KW Immunoglobulin V region; Signal.
 FT CHAIN 1 19
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DISULFID 86 117 FRAMEWORK 3.
 FT NON_TER 117 117 BY SIMILARITY.

FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 66.1%; Score 422; DB 1; Length 117;
 Best Local Similarity 79.6%; Pred. No. 3.1e-37;
 Matches 78; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 1 EVOLQOSGAEELVKGASVSKSCASGYFTNYFYWVKORPGGLEWIGETINPRNGDTDF 60
 DB 20 EVOLQOSGAEELVKGASVSKSCASGYFTNYFYWVKORPGGLEWIGETINPRNGDTDF 79
 QY 61 NEKFESEATLVYDKSSSTAYWQLSLTSEDSAYVYC 98
 DB 80 NEKFESEATLVYDKSSSTAYWQLSLTSEDSAYVYC 117

RESULT 15
 ID HV10_MOUSE STANDARD; PRT; 117 AA.
 AC P01754; P11270;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 IG HEAVY CHAIN V REGION 145 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6;
 RX MEDLINE-81234548; PubMed-6788376;
 RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
 RT "heavy chain variable region contribution to the NpB family of antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
 DR PIR: J00533; AAA38602.1; -.
 DR PIR: C02034; HVMS45.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; 1g; 1.
 KW Immunoglobulin V region; Signal.
 FT CHAIN 1 19
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DISULFID 86 117 FRAMEWORK 3.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;

Query Match 65.5%; Score 418; DB 1; Length 117;
 Best Local Similarity 79.6%; Pred. No. 8.1e-37;
 Matches 78; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 1 EVOLQOSGAEELVKGASVSKSCASGYFTNYFYWVKORPGGLEWIGETINPRNGDTDF 60
 DB 20 EVOLQOSGAEELVKGASVSKSCASGYFTNYFYWVKORPGGLEWIGETINPRNGDTDF 79

Thu Jun 21 10:32:46 2001

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Page 7

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Qy      61 NEKESRATLTVDKSSSTAYMQLSLTSEDSAYYYCTR  98
      |||:::||||| ||||| ||||| ||||| ||||| |||||
Db      80 NEKFSKATLTVDKPSSSTAYMQLSLTSEDSAVYYCAR  117
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Search completed: June 20, 2001, 11:18:56
Job time: 307 sec

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OM protein - protein search, using sw model

Run on: June 20, 2001, 10:47:39 ; Search time 61.83 Seconds

(without alignments)
147,840 Million cell updates/sec

Title: US-09-615-872-1

Sequence: 1 EVQLQSGAEELVKPGASVKL.....YGNNGFTYWGQGLTVTSA 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR68:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	509.5	79.9	116	2 S55542	Ig heavy chain V r
2	498.5	78.1	138	2 S21810	Ig heavy chain V r
3	492	77.1	120	2 S41394	Ig heavy chain V r
4	486	76.2	126	2 S31930	Ig gamma chain pre
5	485	76.0	139	1 MHMS18	Ig heavy chain pre
6	483	75.7	118	2 PC4402	peib leader/Ig hea
7	483	75.7	139	2 C30560	Ig heavy chain V r
8	483	75.7	139	2 PS0024	Ig heavy chain pre
9	482.5	75.6	131	2 A27472	Ig heavy chain pre
10	481	75.3	120	2 B27269	Ig heavy chain V r
11	480.5	75.3	138	1 HVMST7	Ig heavy chain pre
12	479.5	75.2	140	2 PH1482	Ig heavy chain V r
13	477	74.8	135	2 A30577	Ig heavy chain pre
14	476.5	74.7	119	2 C30562	Ig heavy chain pre
15	475.5	74.5	140	1 HVMST7	Ig heavy chain V r
16	474.5	74.4	119	2 E30562	Ig heavy chain V r
17	473.5	74.2	117	2 JC2269	Ig heavy chain pre
18	471.5	73.9	120	2 S25175	PL7-6 antibody hea
19	471.5	73.9	123	2 S20646	Ig heavy chain V r
20	471.5	73.9	138	2 E32513	Ig heavy chain pre
21	471	73.8	141	2 JL0076	Ig heavy chain pre
22	469.5	73.6	121	2 A26405	Ig heavy chain pre
23	469	73.5	115	2 A54378	Ig heavy chain V r
24	469	73.5	117	2 S25176	Ig heavy chain V r
25	467.5	73.3	123	2 D30562	Ig heavy chain V r
26	467	73.2	139	2 S60067	Ig heavy chain V r
27	467	73.2	137	2 E29380	Ig heavy chain pre
28	466.5	73.1	118	2 S38565	Ig heavy chain V r
29	465.5	73.0	119	2 S20640	Ig heavy chain V r

30	465.5	73.0	246	2 S38950	Ig gamma chain - m
31	465.5	73.0	46	2 S40295	Ig gamma-2a chain
32	464.5	72.8	136	2 PL0208	Ig heavy chain pre
33	462.5	72.5	122	2 S20643	Ig heavy chain V r
34	462.5	72.5	135	2 PH1493	Ig heavy chain V r
35	462.5	72.5	140	2 PH1484	Ig heavy chain V r
36	462	72.4	116	2 S53751	antibody Fab Jel 1
37	462	72.4	117	2 B27563	Ig heavy chain V r
38	462	72.4	136	2 JL0077	Ig heavy chain pre
39	461	72.3	113	2 S25041	Ig heavy chain V r
40	461	72.3	135	2 PS0057	Ig heavy chain pre
41	461	72.3	137	2 F29380	Ig heavy chain pre
42	461	72.3	139	2 A27609	Ig heavy chain pre
43	460.5	72.2	125	2 S20639	Ig heavy chain V r
44	460.5	72.2	140	2 PH1489	Ig heavy chain V r
45	460	72.1	113	2 S25044	Ig heavy chain V r

ALIGNMENTS

```

RESULT 1
S55542
Ig heavy chain V region pe2 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C:Accession: S55542
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies u
utations in the variable region genes.
A:Reference number: S55528; MWID:95239763
A:Accession: S55542
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <BOE>
A:Cross-references: EMBL:X82581; NID:9854302; PIDN:CAA57917.1; PID:9854303
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:14-97/Domain: Immunoglobulin homology <IMM>

Query Match 79.9%; Score 509.5; DB 2; Length 116;
Best Local Similarity 82.4%; Pred. No. 1.1e-39;
Matches 98; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

QY 2 VOLQSGAEELVKPGASVKLSCKASGYTFYTWKORPGGLEWIGELINPRNGDTDFN 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 VOLQSGAEELVKPGASVKLSCKASGYTFYTWKORPGGLEWIGELINPRNGDTDFN 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 EKESRATLVDRKSSSTAYVQSLTSEDAITTCRSPYGNNGFTYWGQGLTVTSA 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 EKESRATLVDRKSSSTAYVQSLTSEDAIVYYCTR--GVVAMSDYWGQGLTVTSS 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 2
S21810
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S21810
R:Stemeyer, M.; Brack, C.H.; Traunecker, A.; Koehler, G.
submitted to the EMBL Data Library, January 1991
A:Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy
A:Reference number: S21810
A:Accession: S21810
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-138 <OST>
A:Cross-references: EMBL:X56936; NID:954163; PIDN:CAA40257.1; PID:954164
C:Genetics:
A:Introns: 15/3
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

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	Query Match	76.0%;	Score 485;	DB 4;	Length 287;	
	Best Local Similarity	76.0%;	Pred. No. 4.8e-37;			
	Matches	92;	Conservative 16;	Mismatches 11;	Indels 2;	Gaps 2.
OY	1 EVOLQSGAELVKKPGASVKLSCKASGYFTNFIYWKVRPQGLEGWIEINPRNDTDF	60				
	:		:::::			:
Db	160 QVQLDQPPAEILTKPKPASVKLSCKASGYYFTSYMMHWKRRPGRGLEIMIGRIDPNSSGTXY	219				
OY	61 NEKEFSRATFLIVDKSSSTAYVMQLSSLTSDSAIYYCTR - SPYGNNNGFTYWGOTLLVTVS	119				
Db	220 NEKFKSRTATFLVDKPSSTAYVMQLSSLTSDSAIYYCARDDYGGSSV - FDYMGOGTLTVTS	278				
OY	120 A 120					
Db	279 S 279					

[illegible]

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RESULT      8
PS0024
Ig heavy chain precursor V region (6A4) - mouse
C: Species: Mus musculus (house mouse)
C: Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Nov-1996
C: Accession: PS0024
R: Mergel, M.; Eckhardt, A.; Ehret, W.; von Specht, B. O.; Duchene, M.; Domdey, H
Range 74, 335-345, 1988

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[illegible]

Query Match	75.6%	Score 482.5	DB 2:	Length 131.
Best Local Similarity	79.1%	Pred. No. 3,6e-37:		
Matches	91:	Conservative 11:	Mismatches 10:	Indels 3:
			Gaps	1

OY	1	EVOLQSSAEVLPRASVKYLSKASGTYFTNTFTWVQKRPQSGLEWELNPRGDDTF	60
	20	QVQLDQPPAEELPPASVKLSKASGTYFTSTMMHWAKORPQGLDMLGEINPSKCRNTY	79
OY	61	NEKEFSRATLTVDKSSSTAYVMOLSLSTEDSAIYYCTRSPYGNMYGFTYWGQGL	115
db	80	NEKEFSKATLTVDKSSSTAYVMOLSLSTEDSAIYYVCASQYD--WFAWAGQGL	131

RESULT 10
B22769
Ig heavy chain V region (B1-8_V1/V2) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996
C:Accession: B22769
R:Dildrop, R.; Brügemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
EMBO J. 1, 633-640, 1982
#:Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 20, 2001, 10:47:39 ; Search time 29.71 Seconds
(without alignments)
81.365 Million cell updates/sec

Title: US-09-615-872-1

Perfect score: 638
Sequence: 1.EVQLQQSGAEIVKPGASVKL.....YGNNGFTYWGQGLTVTVSA 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep:*
- 6: /cgn2_6/ptodata/2/1aa/Backfiles1.pep:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	515.5	80.8	116	US-08-737-560A-7	Sequence 7, Appl
2	507.5	79.5	119	US-08-553-497A-12	Sequence 12, Appl
3	506.5	79.4	119	US-08-737-560A-10	Sequence 10, Appl
4	501	78.5	122	US-08-236-520-9	Sequence 9, Appl
5	501	78.5	122	US-08-553-497A-12	Sequence 12, Appl
6	500.5	78.4	139	US-08-894-922A-5	Sequence 5, Appl
7	500.5	78.4	252	US-08-894-922A-14	Sequence 14, Appl
8	500.5	78.4	271	US-08-894-922A-10	Sequence 10, Appl
9	495.5	77.7	123	US-08-497-312-15	Sequence 15, Appl
10	495.5	77.7	123	US-08-560-558E-28	Sequence 28, Appl
11	493.5	77.4	143	US-08-236-520-7	Sequence 7, Appl
12	493.5	77.4	143	US-08-553-497A-12	Sequence 12, Appl
13	490.5	76.9	145	US-08-353-400-33	Sequence 33, Appl
14	490.5	76.9	146	US-08-353-400-36	Sequence 36, Appl
15	489	76.6	120	US-08-397-411-11	Sequence 11, Appl
16	489	76.6	139	US-08-656-58E-4	Sequence 4, Appl
17	488.5	76.6	244	US-08-553-497A-20	Sequence 20, Appl
18	488.5	76.6	246	US-08-553-497A-24	Sequence 24, Appl
19	488	76.5	269	US-08-428-257A-72	Sequence 72, Appl
20	488	76.5	269	US-08-491-988-3	Sequence 3, Appl
21	488	76.5	402	US-08-491-988-9	Sequence 9, Appl
22	488	76.5	415	US-08-491-988-7	Sequence 7, Appl
23	488	76.5	435	US-08-403-853-18	Sequence 5, Appl
24	486	76.2	273	US-08-553-497A-8	Sequence 8, Appl
25	485.5	76.1	119	US-08-202-047-21	Sequence 21, Appl
26	483	75.7	128	US-08-964-690-21	Sequence 21, Appl
27	483	75.7	128	US-08-964-690-21	Sequence 21, Appl

28	482.5	75.6	244	2	US-08-553-497A-22	Sequence 22, Appl
29	479	75.1	115	2	US-08-672-345C-18	Sequence 18, Appl
30	479	75.1	115	2	US-08-672-345C-108	Sequence 108, Appl
31	477.5	74.8	119	4	US-08-767-128-10	Sequence 10, Appl
32	477.5	74.8	240	1	US-07-946-421-24	Sequence 24, Appl
33	477.5	74.8	242	1	US-08-553-497A-26	Sequence 26, Appl
34	476.5	74.7	119	4	US-08-767-128-6	Sequence 6, Appl
35	476.5	74.7	123	1	US-08-497-312-17	Sequence 17, Appl
36	474.5	74.4	138	1	US-08-482-882-78	Sequence 78, Appl
37	474.5	74.4	138	2	US-08-483-389-78	Sequence 78, Appl
38	474.5	74.4	138	2	US-08-487-113D-78	Sequence 78, Appl
39	474.5	74.4	138	2	US-08-473-503-78	Sequence 78, Appl
40	474.5	74.4	138	2	US-08-483-932-78	Sequence 78, Appl
41	474.5	74.4	138	2	US-08-720-430A-78	Sequence 78, Appl
42	474.5	74.4	138	3	US-08-714-017-78	Sequence 78, Appl
43	474.5	74.4	138	3	US-08-475-680-78	Sequence 78, Appl
44	473	74.1	117	3	US-09-065-059-15	Sequence 15, Appl
45	473	74.1	119	1	US-08-467-393-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-737-560A-7
Sequence 7, Application US/08737560A
Patent No. 592893
GENERAL INFORMATION:
APPLICANT: KANG, Chang-Yuill
APPLICANT: KIM, Joong-Gon
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
SREET: Kwanak-gu
CITY: Seoul
STATE: Seoul
COUNTRY: Republic of Korea
ZIP: 151-057
ADDRESS: KIM, Joong-Gon
SREET: Hanyang Apt. 72-1213, ApguJung-dong, Kangnam-gu
CITY: Seoul
STATE: Seoul
COUNTRY: Republic of Korea
ZIP: 135-110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
COMPUTER: IBM PC/AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737, 560A
FILING DATE: 13-NOV-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 95-8176
FILING DATE: 08-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:


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1  APPLICATION NUMBER:  GB 9504344.4
2  FILING DATE: 03-MAR-1995
3  PRIOR APPLICATION DATA: PCT/GB96/00468
4  APPLICATION NUMBER:
5  FILING DATE: 01-MAR-1996
6  ATTORNEY/AGENT INFORMATION:
7  NAME: Kokulis, Paul K.
8  REGISTRATION NUMBER: 16,773
9  REFERENCE/DOCKET NUMBER: 60113/241261
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: (202)-861-3503
12 TELEFAX: (202)-822-0944
13 INFORMATION FOR SEQ ID NO: 14:
14 SEQUENCE CHARACTERISTICS:
15 LENGTH: 252 amino acids
16 TYPE: amino acid
17 TOPOLOGY: linear
18 MOLECULE TYPE: protein
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Query Match	78.4%	Score 500.5	DB 2	Length 252
Best Local Similarity	80.8%	Pred. No. 1.4e-42		
Matches 97	Conservative 11	Mismatches 9	Indels 3	Gaps 2

0Y	1	EVLQOOGSAELVTRFGASVKYLSCKSGAGTFFNYFVWVKORGOELWIGELINPNEGOTDE	60
	4	QVOLOOGSAELVTRFGASVKYLSCKSGADTFFNYSMMHMKORGOELWIGELINPTNGSTYY	63
0Y	61	NEKEERATLTVDKSSSTAYMOQLSLSSEDSALYYSTRSPRGANNYGTYYKQOGLTVTVSA	120
0b	64	NEKRSKATLTVDKSSSTAYMOQLSLSSEDSALYYCAAR-YGNS--EDYMOOGSTTVTVSS	120

RESULT 8
 US-08-994-922A-10
 Sequence 10, Application US/08894922A
 Patent No. 5863765
 GENERAL INFORMATION:
 APPLICANT: BERRY, Mark John
 APPLICANT: DAVIS, Paul James
 APPLICANT: VAN DER LOOT, Cornelius P.E.
 APPLICANT: WHITEHAM, Garry Clark
 TITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
 STREET: 1100 New York Avenue, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: United States
 ZIP: 20005-3918
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: MS Word
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/894,922A
 FILING DATE: 03-SEP-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9504344.4
 FILING DATE: 03-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB96/00468
 FILING DATE: 01-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Kokulis, Paul K.
 REGISTRATION NUMBER: 16,773
 REFERENCE/DOCKET NUMBER: 60113/241261
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)-861-3503

Query Match	77.78;	Score 495.5;	DB 1;	Length 123;
Best Local Similarity	75.68;	Pred. No. 1.9e-42;		
Matches 93;	Conservative 15;	Mismatches 12;	Indels 3;	Gaps 1

11: 121 VSS 123

Oy	1	EVLQDLSGAEELVLRPGASVKLSCKMGSGYFTNYFLIYWKKRGQGDELMTGELNPNRNGDTL	60
Dd	1	OYLQDLGPAAELVLRPGASVKLSCKMGSGYFTNYFLIYWKKRGQGDELMTGELNPNRSGSNT	60
Oy	61	NKKEFSRAFLTVDKSSSTAYVMQLSLTSEDSALYYCTRSPY--GNNGYFTYWGQGLVT	117
Dd	61	NEKETKTATLVDESSSTAYVMQLSLTSEDSADVAHYCTCRQGLMPFSDSRGDGDFPMWGGITLT	120

```
RESULT 11
US-08-236-520-7
: Sequence 7, Application US/08236520
: Patent No. 5591629
: GENERAL INFORMATION:
: APPLICANT: Rodriguez, Moses
: APPLICANT: Miller, David J.
: TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
: TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.
: STREET: Two Millitia Drive
: CITY: Lexington
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02173
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/236,520
: FILING DATE: 29-APR-1994
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Granahan, Patricia
: REGISTRATION NUMBER: 27,227
: REFERENCE/DOCKET NUMBER: MMV92-01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-861-6240
: TELEFAX: 617-861-9540
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 143 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-236-520-7

Query Match 77.4%; Score 493.5; DB 1; Length 143;
Best Local Similarity 76.9%; Pred. No. 3.6e-42;
Matches 93; Conservative 14; Mismatches 13; Indels 1; Gaps 1;

QY 1 EVQLQDSGEELVKPGASVKLSCKASGYTFYFWYKORPGQGLEWIGETINPRNGDTDF 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVQLQQPETELVKPGASVKLSCKASGYFTSTMMHWVKORPGQGLEWIGINPNSGNTNY 79
QY 61 NEKFSRATLVDRKSSSTAYVQMLSLTSEDSAI-YCYTRSPYGNNGYGYGQGLTVTVS 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NEKFSKATLVDRKSSSTAYVQMLSLTSEDSAVYYIARARAYGSRNDYNGQGTTLTVS 139
QY 120 A 120
Db 140 S 140

RESULT 12
PCT-US95-05262-7
: Sequence 7, Application PC/TUS9505262
: GENERAL INFORMATION:
: APPLICANT: Mayo Foundation for Medical Education Research
: TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
: TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.
: STREET: Two Millitia Drive
: CITY: Lexington
: STATE: Massachusetts
```

```
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05262
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/236,520
FILING DATE: April 29, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 27,227
REFERENCE/DOCKET NUMBER: MMV92-01 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 143 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-05262-7

Query Match 77.4%; Score 493.5; DB 5; Length 143;
Best Local Similarity 76.9%; Pred. No. 3.6e-42;
Matches 93; Conservative 14; Mismatches 13; Indels 1; Gaps 1;

QY 1 EVQLQDSGEELVKPGASVKLSCKASGYTFYFWYKORPGQGLEWIGETINPRNGDTDF 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVQLQQPETELVKPGASVKLSCKASGYFTSTMMHWVKORPGQGLEWIGINPNSGNTNY 79
QY 61 NEKFSRATLVDRKSSSTAYVQMLSLTSEDSAI-YCYTRSPYGNNGYGYGQGLTVTVS 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NEKFSKATLVDRKSSSTAYVQMLSLTSEDSAVYYIARARAYGSRNDYNGQGTTLTVS 139
QY 120 A 120
Db 140 S 140

RESULT 13
US-08-353-400-33
: Sequence 33, Application US/08353400
: Patent No. 5665357
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: PROTEINS
: NUMBER OF SEQUENCES: 37
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25 (ERO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/353,400
: FILING DATE:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9324819.3
: FILING DATE: 03-DEC-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9411089.7
: FILING DATE: 03-JUN-1994
: INFORMATION FOR SEQ ID NO: 33:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 445 amino acids
```

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;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-353-400-33

```

[illegible]

RESULT 14
US-08-353-400-36
; Sequence 36, Application US/08353400

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1  GENERAL INFORMATION:
2  APPLICANT:
3  TITLE OF INVENTION: PROTEINS
4  NUMBER OF SEQUENCES: 37
5  COMPUTER READABLE FORM:
6  MEDIUM TYPE: Floppy disk
7  COMPUTER: IBM PC compatible
8  OPERATING SYSTEM: PC-DOS/MS-DOS
9  SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/08/353,400

```

```

1 CLASSIFICATION: 424
2
3 PRIOR APPLICATION DATA:
4
5 APPLICATION NUMBER: GB 9324819.3
6
7 FILING DATE: 03-DEC-1993
8
9 PRIOR APPLICATION DATA:
10
11 APPLICATION NUMBER: GB 9411089.7
12
13 FILING DATE: 03-JUN-1994
14
15 INFORMATION FOR SEQ ID NO: 36:
16
17     SEQUENCE CHARACTERISTICS:
18
19         LENGTH: 464 amino acids
20
21         TYPE: amino acid
22
23         STRANDEDNESS: single
24
25         TOPOLOGY: linear
26
27     MOLECULE TYPE: protein
28
29     OS-08-353-400-36

```

[illegible]

QY	120	A	120
		:	
Db	140	S	140

APPLICANT: Weiner, George
 APPLICANT: Ginglich, Roger
 APPLICANT: Link, Brian
 APPLICANT: Tso, J. Yun
 TITLE OF INVENTION: Bispecific Antibody Effective to Treat
 T-CELL OF INVENTION: B-Cell Lymphoma and Cell Line
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew
 STREET: One Market Plaza, Stewart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA

```

1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Floppy disk
3  COMPUTER: IBM PC compatible
4  OPERATING SYSTEM: PC-DOS/MS-DOS
5  SOFTWARE: PatentIn Release #1.0, Version #1.25
6  CURRENT APPLICATION DATA:
7  APPLICATION NUMBER: US/08/397,411

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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-0049001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400

```

: INFORMATION FOR SEQ ID NO: 11:
:
: SEQUENCE CHARACTERISTICS:
:
:   LENGTH: 120 amino acids
:   TYPE: amino acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
:   MOLECULE TYPE: peptide
:
: OS-08-397-411-11

```

[illegible]

Search completed: June 20, 2001, 11:14:11
Job time: 1592 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2001, 10:47:39 ; Search time 66.12 seconds

(without alignments)
103.745 Million cell updates/sec

Title: US-09-615-872-1

Perfect score: 638

Sequence: 1 EVQLQSGAEIVKRGASVYL.....YGNNGFTYMGQGLTVTSA 120

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

A.Geneseq_0401:*

- 1: /SID56/gcgdata/geneseq/AA1980.DAT:*
- 2: /SID56/gcgdata/geneseq/AA1981.DAT:*
- 3: /SID56/gcgdata/geneseq/AA1982.DAT:*
- 4: /SID56/gcgdata/geneseq/AA1983.DAT:*
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- 20: /SID56/gcgdata/geneseq/AA1999.DAT:*
- 21: /SID56/gcgdata/geneseq/AA2000.DAT:*
- 22: /SID56/gcgdata/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	511	80.1	256	13	R22568	ScFvB18 construct.
2	511	80.1	256	13	R22582	ScFvB18 construct.
3	511	80.1	256	13	R22583	ScFvB18 construct.
4	511	80.1	256	13	R22584	ScFvB18 construct.
5	511	80.1	256	13	R22585	ScFvB18 construct.
6	511	80.1	256	13	R22586	ScFvB18 construct.
7	511	80.1	256	13	R22587	ScFvB18 construct.
8	507.5	79.5	119	16	R79863	Anti-BcFR antibody
9	506.5	79.4	119	17	W04332	Heavy chain of mon
10	501	78.5	122	16	R84555	B-cell lymphoma CH
11	500.5	78.4	119	21	V71473	Mouse monoclonal a

12	500.5	78.4	139	17	W02291	FKC-II VH region.
13	500.5	78.4	252	17	W02294	Yeast-FKC-II-KEX2
14	500.5	78.4	271	17	W02293	FKC-II-KEX2. Chi
15	497.5	78.0	136	8	P70624	Sequence encoded b
16	497.5	78.0	136	8	W10584	Anti-hepatitis B h
17	497.5	78.0	136	18	W16340	Mouse-human chimae
18	497.5	78.0	136	18	W10239	Chimeric anti-hepa
19	497.5	78.0	136	19	W47510	Human anti-hepatit
20	497.5	78.0	136	19	W41054	Human anti-hepatit
21	497.5	78.0	136	19	W47517	Human anti-hepatit
22	497.5	78.0	136	20	W89535	Human anti-hepatit
23	495.5	77.7	123	17	R92990	Chimeric anti-hepa
24	493.5	77.4	143	16	R84554	Monoclonal antibod
25	493	77.3	428	18	W24027	Mab SCH94.03 heavy
26	493	77.3	443	18	W24025	Single chain antiq
27	491.5	77.0	288	20	W62743	Single chain antiq
28	491.5	77.0	673	20	W62742	Fusion protein PNG
29	490.5	76.9	445	16	R76085	Plasmid PNG4/55.1s
30	490.5	76.9	464	16	R76088	Mab 55.1 heavy cha
31	489.5	76.7	117	17	R88716	Mouse antibody hea
32	489	76.6	139	19	W36167	Heavy chain variab
33	488.5	76.6	244	16	R79867	Anti-EGFR single c
34	488.5	76.6	244	16	R79873	Anti-EGFR single c
35	488.5	76.6	246	16	R79869	Anti-EGFR single c
36	488	76.5	269	15	R54756	PRAS11 between H1
37	488	76.5	269	15	R56482	ScFv PRAS107 and p
38	488	76.5	402	15	R56485	ScFv PRAS107 and p
39	488	76.5	435	15	R56483	ScFv PRAS108 and p
40	486	76.2	273	15	R52865	Anti-Influenza N10
41	485.5	76.1	119	16	R79861	Anti-EGFR antibody
42	484.5	75.9	242	16	R79872	Anti-EGFR single c
43	484	75.9	415	15	R56484	ScFv PRAS109 and p
44	483.5	75.8	121	16	R74964	Anti-Idiotypic anti
45	483	75.7	159	10	P93079	Heavy chain of mon

ALIGNMENTS

RESULT 1	
ID R22568	standard; Protein: 256 AA.
XX	
AC R22568:	
XX	
DT 21-MAY-1992 (first entry)	
XX	
DE ScFvB18 construct.	
XX	
KW Fd: bacteriophage; gene III: filamentous; phagemid; capsid; coat;	
KW plus: g3p: binding; adsorption; gene VIII: diverse repertoire;	
KW specific binding pairs; replicable genetic display package.	
XX	
OS Synthetic.	
XX	
FT	Location/Qualifiers
FH	Misc-difference 103
FT	/label= mutation
FT	/note= Ala -> Val (VH FR3) x 3 "
FT	Misc-difference 235
FT	/label= mutation
FT	/note= Tyr -> Asp (VL CDR3) x 1 "
FT	Misc-difference 236
FT	/label= mutation
FT	/note= Ser -> Gly (VL CDR3) x 1 "
FT	Misc-difference 242
FT	/label= mutation
FT	/note= Gly -> Ser (VL FR4) x 21; or
FT	Gly -> Asp (VL FR4) x 3 "
FT	Misc-difference 245
FT	/label= mutation
FT	/note= Thr -> Ile (VL FR4) x 1 "
XX	

```

PN W09201047-A.
XX
PD 23-JAN-1992.
XX
XX 10-JUL-1991; 91WO-GB01134.
PE
XX 15-MAY-1991; 91GB-0010549.
PR 10-JUL-1990; 90GB-0015198.
PR 19-OCT-1990; 90GB-0022845.
PR 12-NOV-1990; 90GB-0024503.
PR 06-MAR-1991; 91GB-0004744.
XX
PA (CAMP-) CAMBRIDGE ANTIBODY.
PA (MED-) MED RES COUNCIL.
XX
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Winter GP, Bonnett TP;
XX
DR WPI: 1992-056862/07.
DR N-PSDB: Q21100.
XX
PT Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic
PT display package.
XX
PS Example 38; Fig 44; 209pp; English.
XX
CC The sequence is encoded by an antibody scfv fragment directed
CC against 4-hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of
CC an MAb against NP were separately amplified and reassembled to form
CC the construct, which was then ligated into the fd gene III contg.
CC vector, fdCAT2, derived from fdmps/Xh. (See Q21095). The clone having
CC the scfvB18 sequence fused in frame to gene III was designated
CC fdCAT2scfvB18. Alternatively the fragment was cloned into fdDOGkan
CC (fdCAT2 with the tet gene replaced by a kanamycin resistance gene)
CC to give fdDOGkanscfvB18, or into the phagemid PHEM1 to create PHEM1-
CC scfvB18. The constructs were used to test the effect of using muta-
CC tor strains to increase the diversity of the cloned genes. The
CC strains NR9046mutD5: NR9046 mutD5::Tn10 and NR9046mutT1: NR9046
CC mutT1::Tn10 were constructed by P1 transduction. After 4 rounds of
CC mutation and screening, 40 phage inserts were sequenced. They each
CC displayed single mutations in 6 different positions, five being in
CC the light chain region. More than 70% of the mutations occurred at
CC positions 724 and 725 (of the nucleotide sequence) changing the
CC first Gly in the J segment (framework 4) to Ser (in 21 cases) or Asp
CC (in 3 cases). The mutant fragments had affinities for NP which were
CC comparable to the wild-type scfv fragment (20nM).
CC N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
CC See also R21260-307, 309-311; R22450, 565-581.
XX
SQ Sequence 256 AA;

```

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Query Match      80.1%; Score 511; DB 13; Length 256;
Best Local Similarity 78.3%; Pred. No. 1,7e-37;
Matches 94; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

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OY 1 EVOLQSGAEIVKPGASVRLSCASGYFTVYFIYWKQPGOGLEWIGETINPRNGDTDF 60
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 7 qvqdgqgaeeivkpgasvrlscasgyftfymhwvqgrgrglwvgrldpmsgqtky 66
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 61 NEKESRATLTVDKSSSTAYWQSLTSEDAIYYCTRSPYGNNGYFTYWGQGLVTYVSA 120
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 67 nekfskattlvdkpsstaywqsltsedsaayycarydyssyfydwgqgtlvvts 126
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

```

RESULT 2
R22582
ID R22582 standard; Protein; 256 AA.
XX
AC R22582;
XX

```

```

DT 21-MAY-1992 (first entry)
XX
DE scfvB18 construct mutant #1.
XX
XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
XX plus; g3p; binding; adsorption; gene VIII; diverse repertoire;
XX specific binding pairs; replicable genetic display package.
XX
OS Synthetic.
XX
FH Key location/Qualifiers
FT Misc-difference 103
FT /label= mutation
FT /note=" Ala -> Val (VH FR3) "
XX
XX W09201047-A.
XX
PD 23-JAN-1992.
XX
XX 10-JUL-1991; 91WO-GB01134.
PE
XX 15-MAY-1991; 91GB-0010549.
PR 10-JUL-1990; 90GB-0015198.
PR 19-OCT-1990; 90GB-0022845.
PR 12-NOV-1990; 90GB-0024503.
PR 06-MAR-1991; 91GB-0004744.
XX
PA (CAMP-) CAMBRIDGE ANTIBODY.
PA (MED-) MED RES COUNCIL.
XX
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Winter GP, Bonnett TP;
XX
DR WPI: 1992-056862/07.
DR N-PSDB: Q23858.
XX
PT Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic
PT display package.
XX
PS Example 38; Fig 44; 209pp; English.
XX
CC The sequence is encoded by an antibody scfv fragment directed
CC against 4-hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of
CC an MAb against NP were separately amplified and reassembled to form
CC the construct, which was then ligated into the fd gene III contg.
CC vector, fdCAT2, derived from fdmps/Xh. (See Q21095). The clone having
CC the scfvB18 sequence fused in frame to gene III was designated
CC fdCAT2scfvB18. Alternatively the fragment was cloned into fdDOGkan
CC (fdCAT2 with the tet gene replaced by a kanamycin resistance gene)
CC to give fdDOGkanscfvB18, or into the phagemid PHEM1 to create PHEM1-
CC scfvB18. The constructs were used to test the effect of using muta-
CC tor strains to increase the diversity of the cloned genes. The
CC strains NR9046mutD5: NR9046 mutD5::Tn10 and NR9046mutT1: NR9046
CC mutT1::Tn10 were constructed by P1 transduction. After 4 rounds of
CC mutation and screening, 40 phage inserts were sequenced. They each
CC displayed single mutations in 6 different positions, five being in
CC the light chain region. More than 70% of the mutations occurred at
CC positions 724 and 725 (of the nucleotide sequence) changing the
CC first Gly in the J segment (framework 4) to Ser (in 21 cases) or Asp
CC (in 3 cases). The mutant shown here occurred three times. The
CC mutant fragments had affinities for NP which were comparable to the
CC wild-type scfv fragment (20nM).
CC N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
CC See also R21260-307, 309-311; R22450, 565-581.
XX
SQ Sequence 256 AA;

```

```

Query Match      80.1%; Score 511; DB 13; Length 256;
Best Local Similarity 78.3%; Pred. No. 1,7e-37;
Matches 94; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

```

```

QY      1  EVOLQSGAELVKGASVRLSKASGYTFNFYIYWKORPGGLEWIGELINPNDGDTDF 60
       :|||||
Db      7  qvqlqsgaelvkgasvrlskasgytftsymhvwkqprgglewigrldpnsqgltky 66
       :|||||
QY      61 NEKFESRATLVYDKSSSTAYMQLSLTSEDSAIYCTRSPYGNNGFTYWGQGLTVTVA 120
       :|||||
Db      67 nekfskaltlvdkpsstaymqjssltssedsavycarydygssyfdywgqglvtvss 126

RESULT  3
R22583  R22583 standard; Protein: 256 AA.
XX
AC      R22583;
XX
DT      21-MAY-1992 (first entry)
XX
DE      scfVb18 construct #2.
XX
KM      fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KM      plus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KM      specific binding pairs; replicable genetic display package.
XX
OS      Synthetic.
XX
FH      Key
FT      Location/Qualifiers
FT      Misc-difference 235
FT      /label= mutation
FT      /note=" Tyr -> Asp (VL CDR3) "
XX
PN      WO9201047-A.
XX
PD      23-JAN-1992.
XX
PF      10-JUL-1991; 91WO-GB01134.
XX
PR      15-MAY-1991; 91GB-0010549.
PR      10-JUL-1990; 90GB-0015198.
PR      19-OCT-1990; 90GB-0022845.
PR      12-NOV-1990; 90GB-0024503.
PR      06-MAR-1991; 91GB-0004744.
XX
PA      (CAMB-) CAMBRIDGE ANTIBODY.
PA      (MED-) MED RES COUNCIL.
XX
PI      McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI      Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI      Winter GP, Bonnett TP;
XX
DR      WPI: 1992-056862/07.
DR      N-PSDB: Q23859.
XX
PT      Producing members of specific binding pairs - by expression in
PT      recombinant host cells with a secreting replicable genetic
PT      display package.
XX
PS      Example 38; Fig 44; 209pp; English.
XX
CC      The sequence is encoded by an antibody scfv fragment directed
CC      against 4-hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of
CC      an mAb against NP were separately amplified and reassembled to form
CC      the construct, which was then ligated into the fd gene III contg.
CC      vector, fdCAT2, derived from fdmps/Xh. (See Q21095). The clone having
CC      the scfVb18 sequence fused in frame to gene III was designated
CC      fdCAT2scfVb18. Alternatively the fragment was cloned into fdDOCKan
CC      (fdCAT2 with the tet gene replaced by a kanamycin resistance gene)
CC      to give fdDOCKanscfVb18, or into the phagemid pHEM1 to create pHEM1-
CC      scfVb18. The constructs were used to test the effect of using muta-
CC      tor strains to increase the diversity of the cloned genes. The
CC      strains NR9046mut5: NR9046 mut5::Tn10 and NR9046mut1: NR9046
CC      mut1::Tn10 were constructed by plasmid transduction. After 4 rounds of
CC      mutation and screening, 40 phage inserts were sequenced. They each

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```

CC      displayed single mutations in 6 different positions, five being in
CC      the light chain region. More than 70% of the mutations occurred at
CC      positions 724 and 725 (of the nucleotide sequence) changing the
CC      first Gly in the J segment (framework 4) to Ser (in 21 cases) or Asp
CC      (in 3 cases). The mutant shown here occurred once. The mutant frag-
CC      ments had affinities for NP which were comparable to the wild-type
CC      scfv fragment (20nM).
CC      N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
CC      See also R21260-307, 309-311; R22450, 565-581.
XX
SQ      Sequence 256 AA;
XX
Query Match      80.1%; Score 511; DB 13; Length 256;
Best Local Similarity 78.3%; Pred. No. 1,7e-37;
Matches 94; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

QY      1  EVOLQSGAELVKGASVRLSKASGYTFNFYIYWKORPGGLEWIGELINPNDGDTDF 60
       :|||||
Db      7  qvqlqsgaelvkgasvrlskasgytftsymhvwkqprgglewigrldpnsqgltky 66
       :|||||
QY      61 NEKFESRATLVYDKSSSTAYMQLSLTSEDSAIYCTRSPYGNNGFTYWGQGLTVTVA 120
       :|||||
Db      67 nekfskaltlvdkpsstaymqjssltssedsavycarydygssyfdywgqglvtvss 126

RESULT  4
R22584  R22584 standard; Protein: 256 AA.
XX
AC      R22584;
XX
DT      21-MAY-1992 (first entry)
XX
DE      scfVb18 construct #3.
XX
KM      fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KM      plus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KM      specific binding pairs; replicable genetic display package.
XX
OS      Synthetic.
XX
FH      Key
FT      Location/Qualifiers
FT      Misc-difference 236
FT      /label= mutation
FT      /note=" Ser -> Gly (VL CDR3) "
XX
PN      WO9201047-A.
XX
PD      23-JAN-1992.
XX
PF      10-JUL-1991; 91WO-GB01134.
XX
PR      15-MAY-1991; 91GB-0010549.
PR      10-JUL-1990; 90GB-0015198.
PR      19-OCT-1990; 90GB-0022845.
PR      12-NOV-1990; 90GB-0024503.
PR      06-MAR-1991; 91GB-0004744.
XX
PA      (CAMB-) CAMBRIDGE ANTIBODY.
PA      (MED-) MED RES COUNCIL.
XX
PI      McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI      Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI      Winter GP, Bonnett TP;
XX
DR      WPI: 1992-056862/07.
DR      N-PSDB: Q23860.
XX
PT      Producing members of specific binding pairs - by expression in
PT      recombinant host cells with a secreting replicable genetic
PT      display package.
XX

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```
PS Example 38; Fig 44; 209pp; English.
XX
CC The sequence is encoded by an antibody scfv fragment directed
CC against 4-hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of
CC an MAb against NP were separately amplified and reassembled to form
CC the construct, which was then ligated into the fd gene III contg.
CC vector, fdCAT2, derived from fdtps/Xh.(See Q21095). The clone having
CC the scfvB18 sequence fused in frame to gene III was designated
CC fdCAT2scfvB18. Alternatively the fragment was cloned into fdDOCKan
CC (fdCAT2 with the tet gene replaced by a kanamycin resistance gene)
CC to give fdDOCKanscfvB18, or into the phagemid pHEM1 to create pHEM1-
CC scfvB18. The constructs were used to test the effect of using muta-
CC tor strains to increase the diversity of the cloned genes. The
CC strains NR9046mutD5: NR9046 mutD5::Tn10 and NR9046mutT1: NR9046
CC mutT1::Tn10 were constructed by P1 transduction. After 4 rounds of
CC mutation and screening, 40 phage inserts were sequenced. They each
CC displayed single mutations in 6 different positions, five being in
CC the light chain region. More than 70% of the mutations occurred at
CC positions 724 and 725 (of the nucleotide sequence) changing the
CC first Gly in the J segment (framework 4) to Ser (in 21 cases) or Asp
CC (in 3 cases). The mutant shown here occurred once. The mutant
CC fragments had affinities for NP which were comparable to the wild-
CC type scfv fragment (20nM).
CC N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
CC See also R21260-307, 309-311; R22450, 565-581.
XX
SO Sequence 256 AA;

Query Match 80.1%; Score 511; DB 13; Length 256;
Best Local Similarity 78.3%; Pred. No. 1,76-37;
Matches 94; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

OY 1 EVOLQOAGAEIVKPGASVKLSCKASGYFTYVFIYWKORPGQGLEWIGETINPRNGDTDF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 7 qvqlqgsaaelvkgpaskklscaksgyftfysymhwvkgprgqglwlgtrldpnsqgltky 66
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 NEKESRATLVNDRSSSTAYWQLSLTSEDSAIYYCTRSPYGNNGYFTYWGQGLTVTVSA 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 nekfskaltlvdkpsstaymqsltsedsaavyycarydyssyfdywgqglvtvss 126

RESULT 5
R22585 ID R22585 standard; Protein; 256 AA.
XX
AC R22585;
XX
DT 21-MAY-1992 (first entry)
XX
DE scfvB18 construct #4.
XX
KM Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KM plus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KM specific binding pairs; replicable genetic display package.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 242 /label= mutation
FT FT /note= Gly -> Ser (VL FR4) "
XX
PN MO9201047-A.
XX
PD 23-JAN-1992.
XX
PF 10-JUL-1991; 91WO-GB01134.
XX
PR 15-MAY-1991; 91GB-0010549.
PR 10-JUL-1990; 90GB-0015198.
PR 19-OCT-1990; 90GB-0022845.
PR 12-NOV-1990; 90GB-0024503.
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PR 06-MAR-1991; 91GB-0004744.
XX
PA (CAMP-) CAMBRIDGE ANTIBODY.
PA (MEDT-) MED RES COUNCIL.
XX
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Walter GP, Bonnett TP;
XX
DR WPI: 1992-056862/07.
DR N-PSDB: Q23861.
XX
PT Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic
PT display package.
XX
PS Example 38; Fig 44; 209pp; English.
XX
CC The sequence is encoded by an antibody scfv fragment directed
CC against 4-hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of
CC an MAb against NP were separately amplified and reassembled to form
CC the construct, which was then ligated into the fd gene III contg.
CC vector, fdCAT2, derived from fdtps/Xh.(See Q21095). The clone having
CC the scfvB18 sequence fused in frame to gene III was designated
CC fdCAT2scfvB18. Alternatively the fragment was cloned into fdDOCKan
CC (fdCAT2 with the tet gene replaced by a kanamycin resistance gene)
CC to give fdDOCKanscfvB18, or into the phagemid pHEM1 to create pHEM1-
CC scfvB18. The constructs were used to test the effect of using muta-
CC tor strains to increase the diversity of the cloned genes. The
CC strains NR9046mutD5: NR9046 mutD5::Tn10 and NR9046mutT1: NR9046
CC mutT1::Tn10 were constructed by P1 transduction. After 4 rounds of
CC mutation and screening, 40 phage inserts were sequenced. They each
CC displayed single mutations in 6 different positions, five being in
CC the light chain region. More than 70% of the mutations occurred at
CC positions 724 and 725 (of the nucleotide sequence) changing the
CC first Gly in the J segment (framework 4) to Ser (in 21 cases), as
CC shown here) or Asp (in 3 cases). The mutant fragments had affin-
CC ties for NP which were comparable to the wild-type scfv fragment
CC (20nM).
CC N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
CC See also R21260-307, 309-311; R22450, 565-581.
XX
SO Sequence 256 AA;

Query Match 80.1%; Score 511; DB 13; Length 256;
Best Local Similarity 78.3%; Pred. No. 1,76-37;
Matches 94; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

OY 1 EVOLQOAGAEIVKPGASVKLSCKASGYFTYVFIYWKORPGQGLEWIGETINPRNGDTDF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 7 qvqlqgsaaelvkgpaskklscaksgyftfysymhwvkgprgqglwlgtrldpnsqgltky 66
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 NEKESRATLVNDRSSSTAYWQLSLTSEDSAIYYCTRSPYGNNGYFTYWGQGLTVTVSA 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 nekfskaltlvdkpsstaymqsltsedsaavyycarydyssyfdywgqglvtvss 126

RESULT 6
R22586 ID R22586 standard; Protein; 256 AA.
XX
AC R22586;
XX
DT 21-MAY-1992 (first entry)
XX
DE scfvB18 construct #5.
XX
KM Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KM plus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KM specific binding pairs; replicable genetic display package.
XX
OS Synthetic.
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XX Key Location/Qualifiers
FH MISC-difference 242 /label= mutation
FT /note=" Gly -> Asp (VL FR4) "
XX
XX WO9201047-A.
XX
XX 23-JAN-1992.
XX
XX 10-JUL-1991; 91WO-GB01134.
XX
XX 15-MAY-1991; 91GB-0010549.
XX 10-JUL-1990; 90GB-0015198.
XX 19-OCT-1990; 90GB-0022845.
XX 12-NOV-1990; 90GB-0024503.
XX 06-MAR-1991; 91GB-0004744.
XX
XX (CAMP-) CAMBRIDGE ANTIBODY.
XX (MEDI-) MED RES COUNCIL.
XX
XX McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
XX Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
XX Winter GP, Bonnett TP;
XX
XX MPI: 1992-056862/07.
XX N-PSDB: Q23862.
XX
XX Producing members of specific binding pairs - by expression in
XX recombinant host cells with a secreting replicable genetic
XX display package.
XX
XX Example 38; Fig 44; 209pp; English.
XX
XX The sequence is encoded by an antibody scfv fragment directed
XX against 4-hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of
XX an MAb against NP were separately amplified and reassembled to form
XX the construct, which was then ligated into the fd gene III contg.
XX vector, fdCAT2, derived from fdgfp/Xh. (See Q21095). The clone having
XX the scfVB18 sequence fused in frame to gene III was designated
XX fdCAT2scfVB18. Alternatively the fragment was cloned into fdDOCKan
XX (fdCAT2 with the tet gene replaced by a kanamycin resistance gene)
XX to give fdDOCKanscfVB18, or into the phagemid pHEM1 to create pHEM1-
XX scfVB18. The constructs were used to test the effect of using muta-
XX tor strains to increase the diversity of the cloned genes. The
XX strains NR9046mutD5::Tn10 and NR9046mutT1::NR9046
XX mutT1::Tn10 were constructed by pl transduction. After 4 rounds of
XX mutation and screening, 40 phage inserts were sequenced. They each
XX displayed single mutations in 6 different positions, five being in
XX the light chain region. More than 70% of the mutations occurred at
XX positions 724 and 725 (of the nucleotide sequence) changing the
XX first gly in the J segment (framework 4) to Ser (in 21 cases) or Asp
XX (in 3 cases, as shown here). The mutant fragments had affinities
XX for NP which were comparable to the wild-type scfv fragment (20nM).
XX N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
XX See also R21260-307, 309-311; R22450, 565-581.
XX
XX Sequence 256 AA:
XX
XX Query Match 80.1%; Score 511; DB 13; Length 256;
XX Best Local Similarity 78.3%; Pred. No. 1,7e-37;
XX Matches 94; Conservative 15; Mismatches 11; Indels 0; Gaps 0;
XX
XX 1 EVOLOOSGAEIVKPGASVYLSGASGYTFNFIYVWKRPOGLEWIGEINRNDTDF 60
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 7 gqyldqsgaeiykpgasvxlscasgytltsywmhwktrpgglewlgldpnsqgty 66
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 61 NEKFESRALITVDKSSSTYMOQLSLTSDSAIYCTRTSPGNNNYCFYWGQGLITVSA 120
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX Db 67 nekfkakeltvdkspsstymqjlsitdsavvyrcarydygssyfdywgqglvtvss 126

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RESULT 7
R22587 ID R22587 standard; Protein: 256 AA.
XX AC R22587;
XX
XX 21-MAY-1992 (first entry)
XX
XX ScfVB18 construct #6.
XX
XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
XX plus; g3p; binding; adsorption; gene VIII; diverse repertoire;
XX specific binding pairs; replicable genetic display package.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH MISC-difference 245 /label= mutation
FT /note=" Thr -> Ile (VL FR4) "
XX
XX WO9201047-A.
XX
XX 23-JAN-1992.
XX
XX 10-JUL-1991; 91WO-GB01134.
XX
XX 15-MAY-1991; 91GB-0010549.
XX 10-JUL-1990; 90GB-0015198.
XX 19-OCT-1990; 90GB-0022845.
XX 12-NOV-1990; 90GB-0024503.
XX 06-MAR-1991; 91GB-0004744.
XX
XX (CAMP-) CAMBRIDGE ANTIBODY.
XX (MEDI-) MED RES COUNCIL.
XX
XX McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
XX Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
XX Winter GP, Bonnett TP;
XX
XX MPI: 1992-056862/07.
XX N-PSDB: Q23863.
XX
XX Producing members of specific binding pairs - by expression in
XX recombinant host cells with a secreting replicable genetic
XX display package.
XX
XX Example 38; Fig 44; 209pp; English.
XX
XX The sequence is encoded by an antibody scfv fragment directed
XX against 4-hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of
XX an MAb against NP were separately amplified and reassembled to form
XX the construct, which was then ligated into the fd gene III contg.
XX vector, fdCAT2, derived from fdgfp/Xh. (See Q21095). The clone having
XX the scfVB18 sequence fused in frame to gene III was designated
XX fdCAT2scfVB18. Alternatively the fragment was cloned into fdDOCKan
XX (fdCAT2 with the tet gene replaced by a kanamycin resistance gene)
XX to give fdDOCKanScfVB18, or into the phagemid pHEM1 to create pHEM1-
XX scfVB18. The constructs were used to test the effect of using muta-
XX tor strains to increase the diversity of the cloned genes. The
XX strains NR9046mutD5::NR9046 mutD5::Tn10 and NR9046mutT1::NR9046
XX mutT1::Tn10 were constructed by pl transduction. After 4 rounds of
XX mutation and screening, 40 phage inserts were sequenced. They each
XX displayed single mutations in 6 different positions, five being in
XX the light chain region. More than 70% of the mutations occurred at
XX positions 724 and 725 (of the nucleotide sequence) changing the
XX first gly in the J segment (framework 4) to Ser (in 21 cases) or Asp
XX (in 3 cases). The mutant shown here occurred once. The mutant
XX fragments had affinities for NP which were comparable to the wild-
XX type scfv fragment (20nM).
XX N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
XX See also R21260-307, 309-311; R22450, 565-586.
XX

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[illegible]

Dd		: : :
Oy	61 NEKESRATLVDSSTAYMQLSLSIEDSAIYCTSPYNNYGFTYMGGTLVYTVA	120
Dd	61 ngkfkgkelltvdkssstaymqsltsedsavyycaarsdygssh-fdwgggtltvsvs	119
RESULT	9	
ID	W04332 standard; peptide; 119 AA.	
AC	W04332;	
DT	23-JUN-1997 (first entry)	
DE	Heavy chain of monoclonal antibody 4B4-1-1.	
KX	Antibody: human; heavy chain; variable region; light chain; MAb; 4-1BB;	
KM	T-cell neurosis factor receptor; membrane protein; accessory molecule;	
KW	T-cell; antigen-presenting cell; immune response; rheumatoid arthritis;	
KX	immunosuppressive agent; autoimmune disease; rejection response; therapy;	
XX	organ transplantation.	
OS	Synthetic.	
FH	Key	Location/Qualifiers
FT	Region	31..35 /note= "complementarity determining region 1"
FT	Region	50..66 /note= "complementarity determining region 2"
FT	Region	99..108 /note= "complementarity determining region 3"
PN	W09632495-A1.	
PD	17-OCT-1996.	
Pf	06-APR-1996; 96WO-KR00045.	
PR	08-APR-1995; 95KR-0008176.	
PA	(GLDS) LG CHEM LTD.	
PI	Kang CY, Kim JG;	
DR	WPl: 1996-477145/47.	
N-PSDB:	T38509.	
PT	Monoclonal antibody specific for human 4-1BB - useful as immunospecific agent for treating autoimmune diseases and preventing organ transplant rejection	
Claim 2;	Page 23; 37pp; English.	
W04332 and W04333 represent fragments of the variable regions of the heavy and light chains of the antibody of the invention. This sequence is encoded by nucleotides 109 to 465 of the coding sequence shown in T38509.		
The antibody of the invention (designated 4B4-1-1) is a monoclonal antibody (MAb) specific for human 4-1BB. 4-1BB encodes a member of the tumour necrosis factor receptor family of integral membrane proteins.		
4-1BB is an accessory molecule expressed on the surface of T-cells in the initial stage of activation. The accessory molecules on the T-cell bind to the corresponding ligand on the antigen-presenting cell and this accelerates the activation of the T- and antigen-presenting cells,		
thereby promoting various immune responses. The MAb is specific for human 4-1BB, which is selectively expressed on activated T-cells. The MAb is useful as an immunosuppressive agent. It can be used for the treatment of autoimmune diseases, such as rheumatoid arthritis, and for preventing rejection response after organ transplantation.		
Sequence	119 AA;	

Matches	96: Conservative	12: Mismatches	11: Indels	1: Gaps	1:
Qy	1	EVOLQOQSAELVKKPASVYKLSCKASGTYFTNTNFYIWKVKORPGQGLEWIGELINPRNGDTDF	60		
Db	1	qyqlqgspaeelvkpaspvylsckasgytftssywmhvwkqrpqvlwlelqelnpnqhny	60		
Qy	61	NEKFESRATLVYDKSSSTAYWOLSSLTSEDSALYYCTRSPYGNNGYFTYWGQGLVTYSA	120		
Db	61	nekfkskatlvtvdkssstacaymgllsttsedsavvycaars-ftlarafeaygqglvtysa	119		
RESULT	12				
ID	W02291	standard; Protein; 139 AA.			
XX	XX				
AC	XX	W02291:			
DT	XX	22-NOV-1996 (first entry)			
DE	XX	FVRC-II VH region.			
XX	XX				
KW	XX	Single chain antibody; Fv; FVRC; heavy chain; light chain;			
KX	XX	antibody engineering; peptide hormone; Pichia pastoris.			
OS	XX	Mus musculus.			
XX	XX				
FH	XX	Key Location/Qualifiers			
FT	XX	Peptide 1..22			
FT	XX	/label= PeIb_leader			
FT	XX	Protein 23..139			
FT	XX	/label= FVRC			
XX	XX				
PN	XX	W09627612-A1.			
XX	XX				
PD	XX	12-SEP-1996.			
XX	XX				
PF	XX	01-MAR-1996; 96WO-GB00468.			
XX	XX				
PR	XX	03-MAR-1995; 95GB-0004344.			
XX	XX				
PA	XX	(UNIL) QUEST INT BV.			
PI	XX	Berry MJ, Davis PJ, Van Der Logt CPE, Whitelam GC;			
XX	XX				
DR	XX	WPI: 1996-425380/42.			
XX	XX	N-PSDB: T36906.			
PT	XX	Prodn. of antibody fragments, partic. in yeast - by prodn. of heavy			
PT	XX	and light chains linked by sequence cleavable by host enzyme			
XX	XX				
PS	XX	Disclosure: Fig 8; 53pp: English.			
XX	XX				
XX	XX	FVRC VH (W02291) and VL (W02292) chains are encoded by a DNA			
CC	XX	construct (T36906) assembled in E. coli vector pUC19. FVRC			
CC	XX	is a single-chain antibody that shows specificity for a peptide			
CC	XX	hormone. Novel antibody fragments (see also W02293-94) have			
CC	XX	been constructed in which the FVRC VH and VL chains are separated			
CC	XX	by a KRX2-type processing sites, allowing prodn. in yeast, partic.			
CC	XX	Pichia pastoris, host cells.			
XX	XX				
SO	XX	Sequence 139 AA:			
Query Match	78.4%;	Score 500.5; DB 17; Length 139;			
Best Local Similarity	80.8%;	Pred. No. 7.5e-37;			
Matches 97; Conservative 11; Mismatches 9; Indels 3; Gaps 2					
Qy	1	EVOLQOQSAELVKKPASVYKLSCKASGTYFTNTNFYIWKVKORPGQGLEWIGELINPRNGDTDF	60		
Db	23	qyqlqgspaeelvkpaspvylsckasdytftssywmhvwkqrpqglwlelqelnpnqhny	82		
Qy	61	NEKFESRATLVYDKSSSTAYWOLSSLTSEDSALYYCTRSPYGNNGYFTYWGQGLVTYSA	120		

```

Db      83 nekfskcatlvcdkssstaymqlssltseedsavvyarr-ygn--fdywgqgtltvrs 139
RESULT 13
ID      W02294
AC      W02294 standard; Protein; 252 AA.
XX
XX      W02294;
XX
XX      22-NOV-1996 (first entry)
XX
XX      Yeast-FVKC-II-KEX2.
XX
XX      Single chain antibody; Fv; FVKC; heavy chain; light chain;
KW      antibody engineering; peptide hormone; Pichia pastoris; KEX2.
XX
XX      Chimeric Mus musculus;
OS      Chimeric synthetic.
XX
XX      Key
FH      Location/Qualifiers
FH      1..120
FH      Domain
FH      /label= VHKC
FH      121..125
FH      Cleavage-site
FH      /note= "KEX2 cleavage site"
FH      Domain
FH      126..239
FH      /label= VHKC
FH      240..252
FH      Peptide
FH      /label= Hydrophil-II-tag
FH      /note= "facilitates Fv assay"
XX
XX      W09627612-A1.
XX
XX      12-SEP-1996.
XX
XX      01-MAR-1996; 96WO-GB00468.
XX
XX      03-MAR-1995; 95GB-0004344.
XX
XX      (UNIL ) QUEST INT BV.
XX
XX      Berry MJ, Davis PJ, Van Der Loft CPE, Whitelam GC;
XX
XX      MPI: 1996-425380/42.
XX      N-PSDB: T36908.
XX      P-PSDB: W02292.
XX
XX      Prod. of antibody fragments, partic. in yeast - by prod. of heavy
XX      and light chains linked by sequence cleavable by host enzyme
XX
XX      Disclosure; Fig 10; 53pp; English.
XX
XX      Yeast-FVKC-II-KEX2 (W02294) comprises a KEX2-type processing site
XX      positioned between the VH and VL chains of peptide hormone-specific
XX      FvHK (see also W02291-92). DNA (T36908) coding for
XX      Yeast-FVKC-II-KEX2 can be incorporated into vector pPIC9 for prodn.
XX      of FvKC-II-KEX2 in Pichia pastoris. This illustrates a process for
XX      prodn. of antibody fragments in which the VH and LH regions are
XX      linked by a sequence cleavable by a host enzyme. The VH and VL are
XX      produced by the yeast in equal amounts as separate chains which are
XX      free to associate and fold.
XX
XX      Sequence 252 AA;
XX
Query Match 78.4%; Score 500.5; DB 17; Length 252;
Best Local Similarity 80.8%; Pred. No. 1,4e-36;
Matches 97; Conservative 11; Mismatches 9; Indels 3; Gaps 2;
1 EVOL00SGAELVKPASVYKLSCKASGYTFNTFIYVWKORPQSGILEWIGELINPRNGDTDF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 11
Db      4 qydlqsgagelrkpdpvslkscaedytltsymhmwvkqrpqgilewgeinplnptgrty 63
61 NEKFSRATLVYDKSSSTAYMQLSSLTSEDSALYYCTNSPYNNTGFTIYWGQGLTVYSA 120

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2001, 11:18:20 ; Search time 107.93 Seconds
(without alignments)
134.843 Million cell updates/sec

Title: US-09-615-872-2
Perfect score: 575
Sequence: 1 AEDIDQMISQKFMSTSVGD.....CQYNSYPLRTGTGKLEIK 110

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP:archaea:*
2: SP:bacteria:*
3: SP:fungi:*
4: SP:human:*
5: SP_invertebrate:*
6: SP:mammal:*
7: SP:mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_unclassified:*
13: SP_vertebrate:*
14: SP_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	386	67.1	108	4 Q9UL70	Q9ul70 homo sapien
2	383	66.6	99	11 Q9UL74	Q9j174 mus musculu
3	367	63.8	108	4 Q9UL79	Q9ul79 homo sapien
4	364	63.3	108	4 Q9UL77	Q9ul77 homo sapien
5	356.5	62.0	109	4 Q9UL85	Q9ul85 homo sapien
6	356	61.9	108	4 Q9UL83	Q9ul83 homo sapien
7	355.5	61.8	107	4 Q9UL81	Q9ul81 homo sapien
8	348.5	60.6	109	4 Q9UL78	Q9ul78 homo sapien
9	344	59.8	107	11 Q9ER29	Q9er29 mus musculu
10	342	59.5	214	11 Q9RI45	Q9ri45 mus musculu
11	323	56.2	107	11 Q9UL84	Q9ul84 mus musculu
12	315.5	54.9	109	4 Q9UL86	Q9ul86 mus musculu
13	313.5	54.5	106	5 Q9UL10	Q9ul10 schistosoma
14	310	53.9	298	11 Q9QYF0	Q9qyf0 mus musculu
15	308.5	53.7	104	11 Q9UL82	Q9ul82 mus musculu
16	296	51.5	103	11 Q9UL80	Q9ul80 mus musculu
17	287	49.9	97	11 Q9UL76	Q9ul76 mus musculu
18	287	49.9	101	11 Q9UL78	Q9ul78 mus musculu
19	276	48.0	114	4 Q9UL80	Q9ul80 homo sapien

20	254	44.2	109	6 Q9NDM5	Q9ndm5 cryotolagus
21	227	39.5	107	4 Q9NSD6	Q9nsd6 homo sapien
22	205.5	35.7	107	4 Q9UL82	Q9ul82 homo sapien
23	179	31.1	109	11 Q9ET13	Q9et13 mus musculu
24	159	27.7	130	4 Q9NP29	Q9np29 homo sapien
25	137.5	23.9	334	13 Q9IB05	Q9ib05 spherooides
26	134	23.3	135	4 Q9H524	Q9h524 homo sapien
27	132.5	23.0	93	4 Q9UL76	Q9ul76 homo sapien
28	130.5	22.7	123	11 Q61243	Q61243 mus musculu
29	130.5	22.7	337	13 Q9IB02	Q9ib02 spherooides
30	122	21.2	235	4 Q9H101	Q9h101 homo sapien
31	119	20.7	320	13 Q9IA29	Q9ia29 spherooides
32	110.5	19.2	337	13 Q9IA24	Q9ia24 spherooides
33	107	18.6	372	4 Q9Y4V0	Q9y4v0 homo sapien
34	106.5	18.5	122	4 Q9G604	Q9g604 homo sapien
35	106	18.4	361	4 Q9H105	Q9h105 homo sapien
36	105.5	18.3	122	4 Q9G603	Q9g603 homo sapien
37	105.5	18.3	137	4 Q9UDR1	Q9udr1 homo sapien
38	105	18.3	342	13 Q9IB00	Q9ib00 spherooides
39	103.5	18.0	503	4 P78324	P78324 homo sapien
40	103.5	18.0	509	11 Q08907	Q08907 mus musculu
41	103	17.9	168	4 Q9Q056	Q9q056 homo sapien
42	102.5	17.8	509	11 Q9QX57	Q9qx57 mus musculu
43	102.5	17.8	513	11 P97797	P97797 mus musculu
44	102	17.7	398	4 Q00241	Q00241 homo sapien
45	100.5	17.5	333	13 Q9IB04	Q9ib04 spherooides

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	108 AA.
ID	Q9UL70			
AC	Q9UL70;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9827139; PubMed=9614934;			
RA	Wu X., Liu B., Van der Werf P.L., Kalls N.N., Berney S.M.,			
RA	Young D.C.;			
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal			
RT	fetus.";			
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).			
CC	-I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX			
CC	DOMAIN.			
DR	EMBL: AF035044; AAD56280.1; -			
DR	HSSP: P01607; 1RET			
DR	InterPro: IPR003006; -			
DR	InterPro: IPR003596; -			
DR	Pfam: PF00047; 1g; 1.			
DR	SMART: SM00406; IGV; 1.			
FT	NON_TER 1			
FT	NON_TER 108			
SO	SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;			

Query Match 67.1%; Score 386; DB 4; Length 108;
Best Local Similarity 67.1%; Pred. No. 2.9e-34;
Matches 72; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY	4	DIGMISQKFMSTSVGDRTVTCKASQNGFTNVAWQQRKFGSPNALITYSARYSGVDP 63
DB	1	DIGMISQKFMSTSVGDRTVTCKASQNGFTNVAWQQRKFGSPNALITYSARYSGVDP 60
QY	64	RTGSGSGTDFLTITNVQSEDLADYFCQYNSYPLRTGTGKLEIK 110

DB 61 RFGSGSGTDFLTITSLQPEDVATYCOQKYNASAPRTFGGKLEIK 107

RESULT 2

09UL74 PRELIMINARY; PRT: 99 AA.

AC 09UL74: 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 OS ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RN NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/C;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
 acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
 RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF206032; AAF69330.1; -
 DR InterPro; IPR003006; -
 DR InterPro; IPR003596; -
 DR Pfam; PF00047; 1g; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 99
 FT SEQUENCE 99 AA; 10939 MW; 3B25D0E78453324 CRC64;

Query Match 66.6%; Score 383; DB 11; Length 99;
 Best Local Similarity 74.7%; Pred. No. 5.5e-34;
 Matches 74; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 12 KMSITSVGDRVTYTCASQNVGTVNVAWYQKPGQSPNALIYSASRYSGVDPRTGSGG 71
 DB 1 KRLVASAGRVTITCKASQSVSNDAWYQKPGQSKLITYASNRKYGVPDRFGSGYG 60
 QY 72 TDFLTITNVOSEDLADYFCQQVNSYPLTFGTGKLEIK 110
 DB 61 TDFLTITNVOSEDLADYFCQQVNSYPLTFGTGKLEIK 99

RESULT 3

09UL79 PRELIMINARY; PRT: 108 AA.

AC 09UL79: 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 OS MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 CC Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus".
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 CC -i- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 DOMAIN.

DR EMBL; AF035035; AAD56271.1; -
 DR HSP; P01607; IREI.
 DR InterPro; IPR003006; -
 DR InterPro; IPR003596; -
 DR Pfam; PF00047; 1g; 1.

DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 108
 FT SEQUENCE 108 AA; 11787 MW; DB5845F19724FBAB CRC64;

Query Match 63.8%; Score 367; DB 4; Length 108;
 Best Local Similarity 63.6%; Pred. No. 3.2e-32;
 Matches 68; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 4 DIQMIOQKFNSTVGDVYTCASQNVGTVNVAWYQKPGQSPNALIYSASRYSGVDP 63
 DB 1 DIVMQSPSLASVGDVYTCASQNVGTVNVAWYQKPGKAPPELLIYASTLQSGVPS 60
 QY 64 RFTGSGSGTDFLTITNVOSEDLADYFCQQVNSYPLTFGTGKLEIK 110
 DB 61 RFGSGSGTDFLTITSLQPEDVATYCOQKYNASAPRTFGGKLEIK 107

RESULT 4

09UL77 PRELIMINARY; PRT: 108 AA.

AC 09UL77: 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 OS MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 CC Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus".
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 CC -i- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 DOMAIN.
 DR EMBL; AF035037; AAD56273.1; -
 DR HSP; P01607; IREI.
 DR InterPro; IPR003006; -
 DR InterPro; IPR003596; -
 DR Pfam; PF00047; 1g; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 108
 FT SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 63.3%; Score 364; DB 4; Length 108;
 Best Local Similarity 64.5%; Pred. No. 6.8e-32;
 Matches 69; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY 4 DIQMIOQKFNSTVGDVYTCASQNVGTVNVAWYQKPGQSPNALIYSASRYSGVDP 63
 DB 1 DIQMIOQKFNSTVGDVYTCASQNVGTVNVAWYQKPGKAPPELLIYASTLQSGVPS 60
 QY 64 RFTGSGSGTDFLTITNVOSEDLADYFCQQVNSYPLTFGTGKLEIK 110
 DB 61 RFGSGSGTDFLTITSLQPEDVATYCOQKYNASAPRTFGGKLEIK 107

RESULT 5

09UL85 PRELIMINARY; PRT: 109 AA.

AC 09UL85: 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 OS MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 CC

SO SEQUENCE 107 AA: 11648 MW: ACF9B1253ACA1E5D CRC64;

Query Match 56.2%; Score 323; DB 11; Length 107;

Best Local Similarity 56.1%; Pred. No. 1.7e-27;

Matches 60; Conservative 15; Mismatches 32; Indels 0; Gaps 0;

OY 4 DIOMIOSOKFMSTVGDRVTVCASQNGTNVAVYQOKPGOSPINALIYASARYSGVPD 63
1 DIOMIOSSTSLASLQDRXXKCSASQISNXXMFQOKPDGTVKLLIYTSLSGVS 60

OY 64 RFTGSGSGTDFLTITNVOSEDLADYFCQYNSYPLTFTGTGKLEIK 110
1 RFTGSGSGADYSLTISNLEPEDIATYCCQYSKFPWTFGGTKLEIK 107

DB 61 RFTGSGSGADYSLTISNLEPEDIATYCCQYSKFPWTFGGTKLEIK 107

RESULT 12
OY0UL86 PRELIMINARY; PRT; 109 AA.

AC OY0UL86; PRELIMINARY; PRT; 109 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_Taxid=9606;

RN NCBI_Taxid=9606;

RP SEQUENCE FROM N.A.

RA MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,

RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus.";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

CC DOMAIN.

DR EMBL: AF035028; AAD56264.1; -.

DR HSSP: P01789; 1MCP.

DR InterPro: IPR003006; -.

DR InterPro: IPR003596; -.

DR Pfam: PF00047; 1g; 1.

DR SMART: SM00406; IGV; 1.

FT NON_TER 1 109

FT SEQUENCE 109 AA: 11928 MW: 243325F72C7DAC83 CRC64;

Query Match 54.9%; Score 315.5; DB 4; Length 109;

Best Local Similarity 55.6%; Pred. No. 1.1e-26;

Matches 60; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

OY 4 DIOMIOSOKFMSTVGDRVTVCASQNGTNVAVYQOKPGOSPINALIYASARYSGVP 62
1 EIVLQSPETLSLPEGERATLSORASQSVSSYLAWYQOKPGAPRLIYGTSSRATGIP 60

OY 63 RFTGSGSGTDFLTITNVOSEDLADYFCQYNSYPLTFTGTGKLEIK 110
1 RFTGSGSGTDFLTITNVOSEDLADYFCQYNSYPLTFTGTGKLEIK 110

DB 61 RFTGSGSGTDFLTITNVOSEDLADYFCQYNSYPLTFTGTGKLEIK 108

RESULT 13
OY0U410 PRELIMINARY; PRT; 106 AA.

AC OY0U410; PRELIMINARY; PRT; 106 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE MONOCLONAL ANTI-IDIDOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN

DE VARIABLE REGION (FRAGMENT).

OS Schistosoma japonicum (Blood fluke).

OC Eukaryota; Metazoa; Platyhelminthes; Rhabdtophora; Neodermata;

OC Trematoda; Digenea; Strigeiidae; Schistosomatidae; Schistosomatidae;

OC Schistosoma.

OX NCBI_Taxid=6182;

RN NCBI_Taxid=6182;

RP SEQUENCE FROM N.A.

RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;

RT "Amplification, cloning and sequence analysis of the light chain

RT variable region gene of monoclonal anti-idiotypic antibody NP30 of

RT Schistosoma japonicum.";

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

CC DOMAIN.

DR EMBL: AF207620; AAF19434.1; -.

DR HSSP: P01679; 2FBJ.

DR InterPro: IPR003008; -.

DR InterPro: IPR003006; -.

DR InterPro: IPR003596; -.

DR Pfam: PF00047; 1g; 1.

DR ProDom: PD00600; -; 1.

DR SMART: SM00406; IGV; 1.

FT NON_TER 1 106

FT SEQUENCE 106 AA: 11478 MW: F20F544426BAE63E CRC64;

Query Match 54.5%; Score 313.5; DB 5; Length 106;

Best Local Similarity 57.7%; Pred. No. 4.8e-26;

Matches 60; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

OY 7 MIOSOKFMSTVGDRVTVCASQNGTNVAVYQOKPGOSPINALIYASARYSGVPDPT 66
1 LQSPAINASPEKEXVTMTCSASSV-SYVWYLOKPGSSPRLIYDTNSLGSVVRFS 62

OY 67 GSGSGTDFLTITNVOSEDLADYFCQYNSYPLTFTGTGKLEIK 110
1 GSGSGTDFLTITNVOSEDLADYFCQYNSYPLTFTGTGKLEIK 110

DB 63 GSGSGTDFLTITNVOSEDLADYFCQYNSYPLTFTGTGKLEIK 106

RESULT 14
OY0YF0 PRELIMINARY; PRT; 298 AA.

AC OY0YF0; PRELIMINARY; PRT; 298 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE CN 8 SCFV.

DE CN 8.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_Taxid=10090;

RN NCBI_Taxid=10090;

RP SEQUENCE FROM N.A.

RA STRAIN-BALB/C; TISSUE-SPLEEN;

RA Shiohara N., Demura T., Fukuda H.;

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

CC [2]

RP SEQUENCE FROM N.A.

RC STRAIN-BALB/C; TISSUE-SPLEEN;

RA Shiohara N., Demura T., Fukuda H.;

RT "Isolation of a novel type of vascular cell wall-specific monoclonal

RT antibody recognizing a cell polarity using a phase display subtraction

RT method.";

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB036341; BAA8633.1; -.

DR HSSP: P01607; 1REI.

DR InterPro: IPR003006; -.

DR InterPro: IPR003596; -.

DR Pfam: PF00047; 1g; 2.

DR SMART: SM00406; IGV; 1.

FT SEQUENCE 298 AA: 31867 MW: E0F96B8A17004317 CRC64;

Query Match	53.9%	Score 310	DB 11	Length 298
Best Local Similarity	53.3%	Pred. NO. 1.5e-25		
Matches 57; Conservative	19	Mismatches 31	Indels 0	Gaps 0

QY 4 DLMQSQKFMSTSGDVRVITTCASQNVGTINAMVQKPGQSPALITYASIRSYGVPD 63
 ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
 Db 173 DIELTQSPASLASYGELVITTCRASGIIHNYLAWYQKQKGSPLLVYNAKTLADGVP 232

QY 64 NRTSGSGTDTLTITNVQSEDLADYFCQQYNSYPLTFGTGKLEIK 110
 ||:||||| :||: ||| | :||| |||||
 Db 233 RFGSGSGTQYSLKINSLQPEDFGSYQCQHFMTTPYTFGGGTKLEIK 279

RESULT 15

ID	Q9JL82	PRELIMINARY;	PRT;	104 AA.
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DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE AATF1-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT)
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxId=10090;
tx

Query Match	53.7%	Score 308.5	DB 11	Length 104
Best Local Similarity	57.8%	Pred. No. 6.1e-26		
Matches	59	Conservative	14	Mismatches 24
				Indels 5
				Gaps 1

```

QY      14  MSTSVGDRVYVTCASQ-----NVGTNAVYQOKPGOSPINALIYSASVRYSGVDPREFYGS  68
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      3  LPVSLGDDQASISCRSSDLSVHTNCTNYLHHYLLQKPGOSPKLITYKVSNNFSGVPDFRFGS  62

```

Qy 69 GSGTDFLTITNVQSEDLADYFCQQYNSYPLTFGTGTGLEIK 110
 ||||| | : : : ||| ||| |
 Db 63 GSGTDFLTIKISRVEAEDLCGYFCSQTHHPYTFGGGTGLEIK 104

Search completed: June 20, 2001, 11:18:21
Job time: 1842 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2001, 11:18:56 ; Search time 33.18 Seconds
(without alignments)
113.566 Million cell updates/sec

Title: US-09-615-872-2

Sequence: 1 AELDIQMISQKFMSTSVGD.....COQYNSYPLFTGCTKLEIK 110

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 93435 seqs, 3425486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	445	77.4	149 1 KV5A_MOUSE	P01633 mus musculu
2	400	69.6	136 1 KV5B_MOUSE	P01634 mus musculu
3	383	66.6	108 1 KV1M_HUMAN	P01605 mus sapien
4	383	66.6	108 1 KV1V_HUMAN	P04430 homo sapien
5	370	64.3	108 1 KV1Y_HUMAN	P80362 homo sapien
6	365	63.5	108 1 KV1E_HUMAN	P01610 homo sapien
7	361	62.8	108 1 KV1F_HUMAN	P01598 homo sapien
8	361	62.8	108 1 KV1G_HUMAN	P01599 homo sapien
9	358.5	62.3	107 1 KV1D_HUMAN	P01596 homo sapien
10	357	62.1	108 1 KV1L_HUMAN	P01604 homo sapien
11	357	62.1	108 1 KV1O_HUMAN	P01600 homo sapien
12	356	61.9	108 1 KV1J_HUMAN	P01608 homo sapien
13	356	61.9	108 1 KV1P_HUMAN	P01611 homo sapien
14	356	61.9	108 1 KV1S_HUMAN	P01607 homo sapien
15	352	61.2	108 1 KV1O_MOUSE	P01632 mus musculu
16	352	61.2	114 1 KV1A_MOUSE	P04431 mus sapien
17	352	61.2	129 1 KV1M_HUMAN	P04207 homo sapien
18	351.5	61.1	129 1 KV1H_HUMAN	P01625 homo sapien
19	351	61.0	114 1 KV4A_HUMAN	P01594 homo sapien
20	350	60.9	108 1 KV1B_HUMAN	P01614 homo sapien
21	347	60.3	134 1 KV4C_HUMAN	P01593 homo sapien
22	346	60.2	108 1 KV1A_HUMAN	P01595 homo sapien
23	345	60.0	108 1 KV1C_HUMAN	P01606 homo sapien
24	345	60.0	108 1 KV1N_HUMAN	P01603 homo sapien
25	343	59.7	108 1 KV1K_HUMAN	P01644 mus musculu
26	343	59.7	108 1 KV5K_MOUSE	P01613 homo sapien
27	342.5	59.6	133 1 KV1B_MOUSE	P01601 homo sapien
28	342	59.5	117 1 KV1I_HUMAN	P01813 homo sapien
29	341.5	59.4	129 1 KV1L_HUMAN	P01622 mus sapien
30	339.5	59.0	109 1 KV5J_MOUSE	P01602 mus musculu
31	339	59.0	108 1 KV1J_MOUSE	P01636 mus musculu
32	339	59.0	117 1 KV1J_HUMAN	P01636 mus musculu
33	338.5	58.9	129 1 KV3M_HUMAN	P01636 mus musculu

34	338	58.8	108 1 KV5L_MOUSE	P01645 mus musculu
35	338	58.8	128 1 KV5E_MOUSE	P01637 mus musculu
36	337	58.6	109 1 KV5P_MOUSE	P01649 mus musculu
37	336.5	58.5	109 1 KV3B_HUMAN	P01620 homo sapien
38	336.5	58.5	109 1 KV3F_HUMAN	P01624 homo sapien
39	336	58.4	108 1 KV5Q_MOUSE	P01650 mus musculu
40	335	58.3	108 1 KV1E_HUMAN	P01597 homo sapien
41	335	58.3	108 1 KV5S_MOUSE	P01652 mus musculu
42	335	58.3	108 1 KV5T_MOUSE	P01653 mus musculu
43	335	58.3	128 1 KV3K_HUMAN	P01631 homo sapien
44	334	58.1	108 1 KV5N_MOUSE	P01647 mus musculu
45	333	57.9	108 1 KV5D_MOUSE	P01636 mus musculu

ALIGNMENTS

RESULT 1
KV5A_MOUSE STANDARD; PRT; 149 AA.
ID KV5A_MOUSE
AC P01633;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE IG KAPPA CHAIN V-V REGION MPC11 PRECURSOR.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE OF 1-71 FROM N.A.
RA MEDLINE=83001944; PubMed=6288267;
RX Kelley D.E., Coleclough C., Perry R.P.;
RT "Functional significance and evolutionary development of the
RT 5'-terminal regions of immunoglobulin variable-region genes."
RL Cell 29:681-689(1982).
RN [2]
RP SEQUENCE OF 41-149 FROM N.A.
RX MEDLINE=80176554; PubMed=6245773;
RA Rabbits T.H., Hamlyn P.H., Matthysens G., Roe B.A.;
RT "The variability, arrangement, and rearrangement of immunoglobulin
RT genes."
RL Can. J. Biochem. 58:176-187(1980).
RN [3]
RP SEQUENCE OF 30-149.
RX MEDLINE=78186617; PubMed=418775;
RA Smith G.P.;
RT "Sequence of the full-length immunoglobulin kappa-chain of mouse
RT myeloma MPC 11."
RL Biochem. J. 171:337-347(1978).
CC -I- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS
CC AMINO END, DUE TO A TANDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE
CC CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL
CC RESIDUE OF TYPICAL KAPPA CHAINS.
CC
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CC
CC EMBL: J00561; AAA38776.1; -
CC PIR: A01916; KVM511.
CC InterPro: IPR003006; -
CC Pfam: pf00047; 19; 1.
KW Immunoglobulin V region; Signal; Duplication.
FT CHAIN 1 29
FT SIGNAL 1 29
FT CHAIN 30 149 IG KAPPA CHAIN V-V REGION MPC11.
FT DOMAIN 42 64 FRAMEWORK 1.
FT DOMAIN 65 75 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 76 90 FRAMEWORK 2.

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FT DOMAIN 91 97 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 98 129 FRAMEWORK 3.
FT DOMAIN 130 138 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 139 148 FRAMEWORK 4.
FT REPEAT 26 35
FT REPEAT 38 47
FT NON_TER 149 149
SQ SEQUENCE 149 AA; 16434 MW; B0480C87B682AC3E CRC64;

Query Match
Best Local Similarity 77.4%; Score 445; DB 1; Length 149;
Matches 85; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

OY 4 DIOMIOSQKFMSTSVGDRVTCTCKASQNGTVNAMYQOKPGQSPNALIYSASRYSGVPD 63
DB 42 DIVMQSHKFMSTSVGDRVTCTCKASQNGTVNAMYQOKPGQSPNALIYSASRYSGVPD 101
OY 64 RFTGSGSGTDFLTITTNVQSEDLADYFCQQVNSYPLTFTGTGKLEIK 110
DB 102 RFTGSGSGTDFLTITTNVQSEDLADYFCQQVNSYPLTFTGTGKLEIK 148

RESULT 2
KV5B_MOUSE STANDARD; PRT; 136 AA.
ID KV5B_MOUSE
AC P01634;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-V REGION MOPC 21 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=82059477; PubMed=6170937;
RA Hamlyn P.H., Galt M.J., Milstein C.;
RT "Complete sequence of an immunoglobulin mRNA using specific priming
RT and the dideoxynucleotide method of RNA sequencing."
RL Nucleic Acids Res. 9:4485-4494(1981).
RN [2]
RP SEQUENCE OF 30-136.
RA MEDLINE=79053310; PubMed=4638343;
RA Svasdi J., Milstein C.;
RT "The complete amino acid sequence of a mouse kappa light chain."
RL Biochem. J. 128:427-444(1972).
CC -----
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CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@sdb.ch).
CC -----
CC EMBL; V00810; CAA24192.1; ALT_TERM.
DR PIR; A01917; KMS21.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; 1g; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 29
FT CHAIN 30 136 IG KAPPA CHAIN V-V REGION MOPC 21.
FT DOMAIN 30 52 FRAMEWORK 1.
FT DOMAIN 53 63 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 64 78 FRAMEWORK 2.
FT DOMAIN 79 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 126 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 127 136 FRAMEWORK 4.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 14902 MW; 8CDD85113996D1C2 CRC64;

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Query Match
Best Local Similarity 69.6%; Score 400; DB 1; Length 136;
Matches 80; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

OY 1 AELDIOMIOSQKFMSTSVGDRVTCTCKASQNGTVNAMYQOKPGQSPNALIYSASRYSG 60
DB 27 ADGNIVMTQSPKSMMSMGERVTLCTCKASENVTVVSMYQOKPEQSPKLLIYGASTREAGVPS 86
OY 61 VDRFTGSGSGTDFLTITTNVQSEDLADYFCQQVNSYPLTFTGTGKLEIK 110
DB 87 VDRFTGSGSGTDFLTITTNVQSEDLADYFCQQVNSYPLTFTGTGKLEIK 136

RESULT 3
KV1M_HUMAN STANDARD; PRT; 108 AA.
ID KV1M_HUMAN
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION LAY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=77036198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT specificities."
RL Scand. J. Immunol. 5:677-684(1976).
CC -----
CC -I- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-II KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01871; KIHULY.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; 1g; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 107 107 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match
Best Local Similarity 66.6%; Score 383; DB 1; Length 108;
Matches 70; Conservative 16; Mismatches 21; Indels 0; Gaps 0;

OY 4 DIOMIOSQKFMSTSVGDRVTCTCKASQNGTVNAMYQOKPGQSPNALIYSASRYSGVPD 63
DB 1 DIOMIOSQKFMSTSVGDRVTCTCKASQNGTVNAMYQOKPGQSPNALIYSASRYSGVPD 60
OY 64 RFTGSGSGTDFLTITTNVQSEDLADYFCQQVNSYPLTFTGTGKLEIK 110
DB 61 RFTGSGSGTDFLTITTNVQSEDLADYFCQQVNSYPLTFTGTGKLEIK 107

RESULT 4
KV1V_HUMAN STANDARD; PRT; 108 AA.
ID KV1V_HUMAN

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AC P04430;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION BAN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=86174817; PubMed=3083240;
 RA Dujlet F.E., O'Connor T.P., Benson M.D.;
 RT "Polymorphism in a kappa I primary (Al) amyloid protein (BAN).";
 RL Mol. Immunol. 23:73-78(1986).
 DR PIR; A01878; KIHUBN.
 DR HSSP; P80362; IWTL.
 DR InterPro; IPR003006;
 DR Pfam; PF00047; Ig; 1.
 DR Immunoglobulin V region; Amyloid.
 KW DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 66.6%; Score 383; DB 1; Length 108;
 Best Local Similarity 66.4%; Pred. No. 2.3e-32;
 Matches 71; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 4 DIOMIOSQKFMSTVSGDRVTTCASQNVGTNVAWQKPGKSPNALIYSASYSGVPD 63
 DB 1 DIQMTSPSSLASVSGDRVTTCRASQSYNYVAMFQKPGKPKSLIDASTLQSGVPS 60

QY 64 RFTGSGSGTDFLTITNVQSEDLADYFCQOQYNSPYLFTGTGLEIK 110
 DB 61 NFGSGSGTDFLTITNVQSEDLADYFCQOQYNSPYLFTGTGLEIK 107
 NCBI_TaxID=9606;

RESULT 5
 KVIY_HUMAN
 ID KVIY_HUMAN STANDARD; PRT; 108 AA.
 AC P80362;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION WAT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RA MEDLINE=95086080; PubMed=7993911;
 RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eultz M.,
 RA Solomon A., Stevens F.J., Schiffer M.;
 RT "Comparison of crystal structures of two homologous proteins:
 RT structural origin of altered domain interactions in immunoglobulin
 RT light-chain dimers.";
 RL Biochemistry 33:14848-14857(1994).
 RN [2]
 RP SEQUENCE OF 1-35.
 RA MEDLINE=81267384; PubMed=6167731;
 RA Stevens F.V., Westholm F.A., Panagiotopoulos N., Schiffer M.,
 RA Popp R.A., Solomon A.;
 RT "Characterization and preliminary crystallographic data on the VL-
 RT related fragment of the human kappa Bence Jones protein WAT.";

RL J. Mol. Biol. 147:185-193(1981).
 CC -I- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
 DR PDB; IWTL; 01-NOV-94.
 DR InterPro; IPR003006;
 DR Pfam; PF00047; Ig; 1.
 DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 KW DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT CONFLICT 30 31 TN -> SD (IN REF. 2).
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match 64.3%; Score 370; DB 1; Length 108;
 Best Local Similarity 62.6%; Pred. No. 4.8e-31;
 Matches 67; Conservative 19; Mismatches 21; Indels 0; Gaps 0;

QY 4 DIOMIOSQKFMSTVSGDRVTTCASQNVGTNVAWQKPGKSPNALIYSASYSGVPD 63
 DB 1 DIQMTSPSSLASVSGDRVTTCRASQSYNYVAMFQKPGKPKSLIDASTLQSGVPS 60

QY 64 RFTGSGSGTDFLTITNVQSEDLADYFCQOQYNSPYLFTGTGLEIK 110
 DB 61 NFGSGSGTDFLTITNVQSEDLADYFCQOQYNSPYLFTGTGLEIK 107
 NCBI_TaxID=9606;

RESULT 6
 KVIY_HUMAN
 ID KVIY_HUMAN STANDARD; PRT; 108 AA.
 AC P01610;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION WEA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=83273707; PubMed=6410398;
 RA Goni F., Frangione B.;
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM
 RT (protein WEA) with antibody activity against 3,4-pyruvylated
 RT galactose in Klebsiella polysaccharides K30 and K33.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
 CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
 CC WALDENSTROM'S MACROGLOBULINEMIA.
 DR PIR; A01876; KIHUWE.
 DR HSSP; P80362; IWTL.
 DR InterPro; IPR003006;
 DR Pfam; PF00047; Ig; 1.
 DR Immunoglobulin V region; Monoclonal antibody.
 KW DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match 63.5%; Score 365; DB 1; Length 108;

[illegible]

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AC P01599
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059122; PubMed=4215718;
RA Laure C.J., Matanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
(macroglublin Gal.), I." The amino acid sequence of the L-chain of
kappa-type subgroup I."
RL Hoppe-Seiler S.Z. Physiol. Chem. 354:1503-1504(1973).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN.
DR PIR; A01867; KIHUGL.
DR HSSP; P01607; 1RET.
DR InterPro: IPR003006;
DR Pfam: PF00047; 1g; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108
SQ SEQUENCE 108 AA; 11814 MW; CIAD3CB0F600FF73 CRC64;

Query Match 62.8%; Score 361; DB 1; Length 108;
Best Local Similarity 61.7%; Pred.No.3.9e-30;
Matches 66; Conservative 18; Mismatches 23; Indels 0; Gaps

QY 4 DIOMISOKFMSTYSVDGRVTVCASQWGVNVMYOOKPGOSPNALITSASYRYSGVPD 63
| | | | : | | | | | : | | | : | | | | | : | | | | |
DB 1 DIGNOTSPSSLASVGDRTTICRASQINDLWMYQOKKCKAKELTIYAASLSGCVPS 60
| | | | | : | | | | : | | : | | : | | : | | | | |
OY 64 RFTGGSGDFITLTINVOSDELADYFCQGYNSPLPFEGTKLEIK 110
| | | | | : | | | | : | | : | | : | | : | | | | |
DB 61 RFSGSAGTEFTLTISLQPEDFAFYCYLOONSYPSPFGOGTRVEIK 107
| | | | | : | | | | : | | : | | : | | : | | | | |

RESULT 9
KVLD_HUMAN STANDARD; PRT; 107 AA.
ID KVID_HUMAN
AC P01596;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION CAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75075135; PubMed=4216454;
RA Milstein C.P., Deverson E.V.;
RT "Primary structure of kappa light chain from a human myeloma
protein."
RL Eur. J. Biochem. 49:377-391(1974).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
PR; A01864; KIH0AR.
```

DR HSP: P80362; 1MTL.
 DR InterPro: IPR003006; -
 DR Pfam: PF00047; 19; 1.
 KW Immunoglobulin V region; Glycoprotein.
 FT CARBOHYD 28
 FT NON_TER 107 107 N-LINKED (GLCNAC. . .)
 SO SEQUENCE 107 AA; 11703 MW; E1BF0DE9844C3346 CRC64;

Query Match 62.3%; Score 358.5; DB 1; Length 107;
 Best Local Similarity 60.7%; Pred. No. 7e-30;
 Matches 65; Conservative 21; Mismatches 20; Indels 1; Gaps 1;

OY 4 DIOMIOSQKFMSTVGDRVTYVCKASQNVAVYQKPGOSPNALISASIRSGVD 63
 DB 1 DIOMTQSPSTLASVGDRAITCRASQNSMLAWYQKPKRAKYLIVKSSLSLEGVPS 60
 OY 64 RFTGSGGTDFLTITNVOSEDLADYFCQOYNSYPLTFGTGTRKLEIK 110
 DB 61 RFTGSGGTDFLTITNVOSEDLADYFCQOYNTF-FTFGPGTRKVDIK 106

RESULT 10
 KY1L_HUMAN STANDARD; PRT; 108 AA.
 ID P01604;
 DT 21-JUL-1986 (rel. 01, Created)
 DT 21-JUL-1986 (rel. 01, Last sequence update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION KUE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79237924; PubMed=112021;
 RA Eultz M., Kley H.-P., Zeidler H.-J.;
 RT "The primary structure of the Bence-Jones protein Kue. The amino acid
 sequence of the variable part of a human L-chain of the kappa-type.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DR PIR: A01870; K1HKU.
 DR HSP: P01607; 1RET.
 DR InterPro: IPR003006; -
 DR Pfam: PF00047; 19; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 3 49 FRAMEWORK 2.
 FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 5 57 FRAMEWORK 3.
 FT DOMAIN 6 88 FRAMEWORK 4.
 FT DISULFID 98 107 FRAMEWORK 4.
 FT NON_TER 23 88 BY SIMILARITY.
 SO SEQUENCE 108 AA; 12127 MW; 906679A5D90FE98 CRC64;

Query Match 62.1%; Score 357; DB 1; Length 108;
 Best Local Similarity 61.7%; Pred. No. 1e-29;
 Matches 66; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

OY 4 DIOMIOSQKFMSTVGDRVTYVCKASQNVAVYQKPGOSPNALISASIRSGVD 63
 DB 1 DIOMTQSPSTLASVGDRAITCRASQNSIMLAWYQKPKRAKYLIVKSSLSLEGVPS 60
 OY 64 RFTGSGGTDFLTITNVOSEDLADYFCQOYNSYPLTFGTGTRKLEIK 110
 DB 61 RFTGSGGTDFLTITNVOSEDLADYFCQOYNSYPLTFGTGTRKLEIK 107

RESULT 11
 KY1Q_HUMAN STANDARD; PRT; 108 AA.
 ID P01609;
 DT 21-JUL-1986 (rel. 01, Created)
 DT 21-JUL-1986 (rel. 01, Last sequence update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION SCW.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=75059271; PubMed=4435756;
 RA Eultz M., Hilschmann N.;
 RT "The primary structure of a human immunoglobulin L-chain of
 kappa-type (Bence-Jones protein SCW). II: The chymotryptic peptides
 and the complete amino acid sequence.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR: A01875; K1HWS.
 DR HSP: P01607; 1RET.
 DR InterPro: IPR003006; -
 DR Pfam: PF00047; 19; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 3 49 FRAMEWORK 2.
 FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 5 57 FRAMEWORK 3.
 FT DOMAIN 6 88 FRAMEWORK 4.
 FT DISULFID 98 107 FRAMEWORK 4.
 FT NON_TER 23 88 BY SIMILARITY.
 SO SEQUENCE 108 AA; 11764 MW; 32CECDDDF9644414 CRC64;

Query Match 62.1%; Score 357; DB 1; Length 108;
 Best Local Similarity 59.8%; Pred. No. 1e-29;
 Matches 64; Conservative 21; Mismatches 22; Indels 0; Gaps 0;

OY 4 DIOMIOSQKFMSTVGDRVTYVCKASQNVAVYQKPGOSPNALISASIRSGVD 63
 DB 1 DIOMTQSPSTLASVGDRAITCRASQNSQDIRKHLNWDQKPKRAKYLIVKSSLSLEGVPS 60
 OY 64 RFTGSGGTDFLTITNVOSEDLADYFCQOYNSYPLTFGTGTRKLEIK 110
 DB 61 RFTGSGGTDFLTITNVOSEDLADYFCQOYNDVPIITFGGTRVEMK 107

RESULT 12
 KY1H_HUMAN STANDARD; PRT; 108 AA.
 ID P01600;
 DT 21-JUL-1986 (rel. 01, Created)
 DT 21-JUL-1986 (rel. 01, Last sequence update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION HAU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=71032830; PubMed=4097974;
 RA Matanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
 chain of subgroup I (Bence-Jones Protein HAU): subdivision within
 RT subgroups.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).

ID KVL0 HUMAN STANDARD: PRT: 108 AA.
AC P01607:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION REI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
kappa-type L-chain, subgroup I (Bence-Jones protein Re1.); Isolation
and characterization of the tryptic peptides; the complete amino acid
sequence of the protein; a contribution to the elucidation of the
three-dimensional structure of antibodies, in particular their
combining site.";
RT Hoppe-seyler's Z. Physiol. Chem. 356:167-191(1975).
RL [2]
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
of the Bence-Jones protein RE1 refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
MARKER.
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01873; KIHURE.
DR PDB: 1REI; 17-FEB-84.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 19; 1.
KM Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT TURN 80 82
FT STRAND 85 90
FT STRAND 98 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9EB143E1188BCE2A CRC64;

Query Match

61.2%; Score 352; DB 1; Length 108;

Best Local Similarity 61.3%; Pred. No. 3.2e-29;

Matches 65; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

4 DIOMIQSGFMTSGVDRVTCTCKASQNGTNVAMVQOKPGOSPNALISASVRYSGVPD 63

||||| : |||||::||::||:: : |||| ||::|| ||| || :|||

DB 1 DIOMIQSGFMTSGVDRVTCTCKASQNGTNVAMVQOKPGOSPNALISASVRYSGVPD 60

OY 64 RFTGSGSGTDFTLTTTNVQSEDLADYPCQOYNSYPLTFGTGTRLEI 109

DB 61 RFTGSGSGTDFTLTTTNVQSEDLADYPCQOYNSYPLTFGTGTRLEI 106

Search completed: June 20, 2001, 11:18:57
Job time: 308 sec

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: June 20, 2001, 11:16:28 ; Search time 61.83 Seconds

(without alignments)
135.520 Million cell updates/sec

Title: US-09-615-872-2

Perfect score: 575

Sequence: 1 AELDIQMISQKFMSTSVGD.....CQOYNSYPLRFCTGKLEIK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

219241

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_68:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	514	89.4	107	2	A28195	Ig kappa chain V r
2	498	86.6	107	2	B28195	Ig kappa chain V r
3	496	86.3	128	2	A47159	Ig lambda chain V
4	484	84.2	108	2	PL0204	anti-DNA autoantib
5	475.5	82.7	108	2	B44371	Ig kappa chain V r
6	474	82.4	98	2	PH1072	Ig light chain V r
7	472	82.1	117	2	S42466	Ig kappa chain V r
8	447	77.7	131	2	PL0207	anti-idiotypic ant
9	445	77.4	107	2	S32192	Ig kappa chain V r
10	445	77.4	149	1	KVMS11	Ig kappa chain pre
11	443	77.0	107	2	S32191	Ig kappa chain V r
12	439	76.3	100	2	H38601	Ig kappa chain V r
13	439	76.3	119	2	PQ0265	Ig kappa chain V r
14	435	73.9	88	2	A37262	Ig kappa chain V r
15	417	72.5	152	2	S30751	Ig kappa chain pre
16	413	71.8	127	2	S04577	Ig kappa chain V r
17	412	71.7	90	2	S38561	Ig light chain V r
18	410.5	71.4	108	2	PL0083	Ig kappa chain V r
19	404	70.3	94	2	F33730	Ig kappa chain V r
20	404	70.3	107	2	S09967	Ig kappa chain V r
21	400	69.6	136	1	KVMS21	Ig kappa chain V-J
22	399	69.4	111	2	D37266	Ig kappa chain pre
23	398	69.2	90	2	I38601	Ig kappa chain V r
24	392	68.2	93	2	S38559	Ig light chain V r
25	382	68.2	132	2	S40334	Ig kappa chain - h
26	381	68.0	125	2	S40333	Ig kappa chain V-J
27	389	67.7	86	2	C28195	Ig kappa chain - h
28	389	67.7	129	2	S40369	Ig kappa chain - h
29	388.5	67.6	225	2	S37484	Ig kappa chain - h

30	388	67.5	125	2	S40353	Ig kappa chain V-J
31	387	67.3	107	2	S38713	Ig light chain V r
32	385	67.0	107	2	S68017	anti-HIV envelope
33	385	67.0	125	2	S40349	Ig kappa chain V-J
34	384	66.8	117	2	S46371	Ig kappa chain V-J
35	383	66.6	108	1	KIHULY	Ig kappa chain V-I
36	383	66.6	108	1	KIHUBN	Ig kappa chain V-I
37	381	66.3	98	2	PH1073	Ig light chain V r
38	381	66.3	145	2	PL0014	Ig kappa chain pre
39	378	65.7	107	2	S33132	Ig kappa chain V r
40	377	65.6	123	2	S40313	Ig kappa chain V-J
41	377	65.6	129	2	S40317	Ig kappa chain - h
42	375.5	65.3	124	2	S40336	Ig kappa chain V-J
43	375	65.2	108	2	S36279	Ig lambda chain V
44	374	65.0	108	2	S40330	Ig kappa chain V-J
45	374	65.0	117	2	S40362	Ig kappa chain - h

ALIGNMENTS

RESULT 1
A28195
Ig kappa chain V region (anti-haloperidol antibody A) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Dec-1989 #sequence-Revision 01-Dec-1989 #text-change 21-Jan-2000
C:Accession: A28195
R:Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino aci
A:Reference number: A28195; MID:88153717
A:Accession: A28195
A:Molecule type: mRNA
A:Residues: 1-107 <SHE>
A:Cross-references: GB:M19766; MID:9197039; PIDN:AAA38891.1; PID:9197040
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 89.4%; Score 514; DB 2; Length 107;
Best local similarity 91.6%; Pred. No. 3.7e-38;
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 4 DIOMISQKFMSTSVGDRTVTCKASQNGTNVAMVQKFGSPNALITSATRYSGVPD 63
DB 1 DIIMTOSQKFMSTSVGDRTVTCKASQNGTNVAMVQKFGSPKALITSATRYSGVPD 60
QY 64 RTFGSSGRTDFTLTINVOSEDLADYFCQOYNSYPLRFCTGKLEIK 110
DB 61 RTFGSSGRTDFTLTINVOSEDLADYFCQOYNSYPLRFCTGKLEIK 107

RESULT 2
B28195
Ig kappa chain V region (anti-haloperidol antibody B) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Dec-1989 #sequence-Revision 01-Dec-1989 #text-change 21-Jan-2000
C:Accession: B28195
R:Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino aci
A:Reference number: A28195; MID:88153717
A:Accession: B28195
A:Molecule type: mRNA
A:Residues: 1-107 <SHE>
A:Cross-references: EMBL:M19767; NID:9197041; PIDN:AAA38892.1; PID:9197042
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 498; DB 2; Length 107;

Ig kappa chain precursor V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
 C:Accession: S30751
 R:Grant, F.J.; Levin, S.D.; Gilbert, T.; Kindsvogel, W.
 Nucleic Acids Res. 15, 5496, 1987
 A:Title: Improved RNA sequencing method to determine immunoglobulin mRNA sequence.
 A:Reference number: S30751; MUID:87260030
 A:Accession: S30751
 A:Molecule type: mRNA
 A:Residues: 1-152 <GRA>
 A:Cross-references: EMBL:X05877; NID:952195; PIDN:CAA29301.1; PID:952196
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:45-119/Domain: immunoglobulin homology <IMM>
 F:138-152/Domain: C region (C-kappa) (fragment) #status predicted <CRE>

Query Match 72.5%; Score 417; DB 2; Length 152;
 Best local Similarity 73.8%; Pred. No. 1.4e-29;
 Matches 79; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

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QY      4 DIQMIOQKFMSTSVGDVTVTCRASONVGTNNAMYOQKPGQSPNALIYSASYRYSGVDP 63
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     30 DIVMTQSHRFMSTSVGDVRSVITCKASQDVTYAVSWYQKPGQSPKLLIFMASTRHRTGVDP 89
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY     64 RFTGSGSGTPTLTITVQSEDLADYFCQOYNSYPLTFGTGKLEIK 110
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     90 RFTGSGSGTPTLTITVQSEDLADYFCQOYNSYPLTFGTGKLEIK 136
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
  
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Search completed: June 20, 2001, 11:16:28
 Job time: 1729 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 20, 2001, 11:14:11 : Search time 29.71 Seconds

(without alignments)
74.585 Million cell updates/sec

Title: US-09-615-872-2

Perfect score: 575
Sequence: 1 AELDIQIQSQKFMSTSVGD.....CQYNSYPLFPGTKLEIK 110

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCRTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	ID	Description
1	517	89.9	127 4	US-08-646-265A-27 Sequence 27, Appl
2	514	89.4	107 4	US-08-767-128-32 Sequence 32, Appl
3	514	89.4	123 1	US-08-398-613A-20 Sequence 20, Appl
4	514	89.4	123 1	US-08-398-612A-20 Sequence 20, Appl
5	514	89.4	123 1	US-08-398-611A-20 Sequence 20, Appl
6	514	89.4	123 2	US-08-491-334A-20 Sequence 20, Appl
7	514	89.4	123 4	US-08-804-444A-17 Sequence 17, Appl
8	514	89.4	123 4	US-08-804-444A-17 Sequence 17, Appl
9	514	89.4	123 4	US-09-026-985-17 Sequence 17, Appl
10	512	89.0	237 1	US-08-398-612A-28 Sequence 28, Appl
11	512	89.0	237 1	US-08-398-611A-28 Sequence 28, Appl
12	512	89.0	237 2	US-08-491-334A-28 Sequence 28, Appl
13	512	89.0	237 3	US-09-027-449-25 Sequence 25, Appl
14	512	89.0	237 4	US-08-804-444A-25 Sequence 25, Appl
15	512	89.0	237 4	US-09-026-985-25 Sequence 25, Appl
16	512	89.0	238 1	US-08-398-613A-28 Sequence 28, Appl
17	495.5	86.2	110 2	US-08-602-725-2 Sequence 2, Appl
18	495.5	86.2	132 2	US-08-602-725-38 Sequence 38, Appl
19	493.5	85.8	124 3	US-08-466-151-4 Sequence 5, Appl
20	490	85.2	131 1	US-08-202-047-5 Sequence 5, Appl
21	490	85.2	131 3	US-08-964-690-5 Sequence 5, Appl
22	488.5	85.0	110 1	US-08-497-312-23 Sequence 23, Appl
23	475.5	82.7	110 1	US-08-497-312-28 Sequence 29, Appl
24	474	82.4	126 4	US-08-646-265A-81 Sequence 81, Appl
25	471.5	82.0	108 2	US-08-657-012-25 Sequence 25, Appl
26	471.5	82.0	108 3	US-09-013-872-25 Sequence 25, Appl
27	471.5	82.0	108 4	US-09-184-198-25 Sequence 25, Appl

28	467	81.2	107 1	US-08-491-845-4 Sequence 4, Appl
29	467	81.2	147 2	US-08-653-402B-4 Sequence 4, Appl
30	466	81.0	126 4	US-08-646-265A-73 Sequence 73, Appl
31	464.5	80.8	110 1	US-08-497-312-25 Sequence 25, Appl
32	464	80.7	107 3	US-08-838-682-19 Sequence 19, Appl
33	464	80.7	107 4	US-08-895-914-19 Sequence 19, Appl
34	464	80.7	108 4	US-08-752-693A-1 Sequence 1, Appl
35	464	80.7	132 1	US-08-253-877C-55 Sequence 55, Appl
36	464	80.7	132 2	US-08-452-164A-55 Sequence 55, Appl
37	463	80.5	237 2	US-08-926-789-16 Sequence 16, Appl
38	463	80.5	237 2	US-08-926-789-16 Sequence 16, Appl
39	463	80.5	241 2	US-08-224-591-18 Sequence 18, Appl
40	463	80.5	241 2	US-08-926-789-18 Sequence 18, Appl
41	459	79.8	126 4	US-08-646-265A-69 Sequence 69, Appl
42	459	79.8	126 4	US-08-646-265A-75 Sequence 75, Appl
43	456	79.3	107 3	US-08-554-840-3 Sequence 3, Appl
44	455	79.1	107 4	US-08-646-265A-131 Sequence 131, App
45	455	79.1	126 4	US-08-646-265A-85 Sequence 85, Appl

ALIGNMENTS

RESULT 1
US-08-646-265A-27
Sequence 27, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25, 258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO.: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-27


```

? APPLICANT: Kim, Kyung Jin
? TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment
? NUMBER OF SEQUENCES: 58
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Genentech, Inc.
? STREET: 460 Point San Bruno Blvd
? CITY: South San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94080
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Winpatin (Genentech)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/398, 611A
? FILING DATE: 01-Mar-1995
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/205864
? FILING DATE: 03-MAR-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Love, Richard B.
? REGISTRATION NUMBER: 34,659
? REFERENCE/DOCKET NUMBER: P0874P1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415/225-5530
? TELEFAX: 415/952-9881
? TELEX: 910/371-7168
? INFORMATION FOR SEQ ID NO.: 20:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 123 amino acids
? TYPE: Amino acid
? TOPOLOGY: Linear
? US-08-398-611A-20

Query Match      89.4%; Score 514; DB 1; Length 123;
Best Local Similarity    90.7%; Pred. No. 2,8e-42;
Matches   97; Conservative     5; Mismatches    5; Indels     0; Gaps       0

Oy      4 DIQMIOQKFMSTVGDRTVTCKASQNNGINVAWTQQKPQGSPNALITSASTRISGVDP 63
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | 
Db      1 DIRMVSQOKFMSTVGDRSVTCRKASKQNNGTNAVWYQKKPGGSKLIYSSTRYSGVPD 60
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | 

Oy      64 RTGGSGGTDFLTITTNVOSEDLADVFCCQYNSSYPFTFGTGRIEIK 110
        ||||| | | | | | | | | : | | | | | | | | | | | | | | | | | | | | 
Db      61 RPTGSAGTDTFLTITSHVQSEDLDLADFCCQNYNIPPLTFGPGRILEIK 107
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | 

RESULT          6
US-08-491-334A-20
Sequence 20, Application US/08491334A
Patent No. 5874080
GENERAL INFORMATION:
APPLICANT: Hebert, Caroline A.
APPLICANT: Kabakoff, Rhona C.
APPLICANT: Moore, Mark W.
TITLE OF INVENTION: IL-8 Antagonists for Treatment of Inflammatory
TITLE OF INVENTION: Disorders and Asthma
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
```



```

; Patent No. 5686070
;
; GENERAL INFORMATION:
;
; APPLICANT: Doershuk, Claire M.
;
; APPLICANT: Fong, Sherman

```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 460 Point San Bruno Blvd
;; CITY: South San Francisco

RESULT	ID	Y44991	standard; Protein: 450 AA.
XX	AC	Y44991;	
XX	DT	23-MAY-2000	(first entry)
XX	DE	M79scFv-interleukin 2-fusion protein containing dimerisation domain.	
KM	KM	Murine; M79 antibody; 17-1A antigen; single-chain Fv fragment; scFv;	
KM	KM	fusion construct; human; interleukin 2; IL-2; dimerisation domain;	
KM	KM	heteroantibody; multifunctional compound; constant domain;	
KM	KM	immunoglobulin; cytosol; immunostimulatory; antileukemia; diagnosis;	
KM	KM	antiproliferative; prevention; treatment; malignant; haematopoietic cell;	
XX	XX	lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.	
OS	OS	Chimeric - Mus sp.	
OS	OS	Chimeric - Homo sapiens.	
XX	XX		
FT	FT	Key	Location/Qualifiers
FT	FT	Peptide	1..19
FT	FT	Region	/label= Leader_peptide
FT	FT	Region	/label= M79scFv_light_chain_variable_region
FT	FT	Region	/label= gly-Ser-linker
FT	FT	Region	/label= M79scFv_heavy_chain_variable_region
FT	FT	Region	/note="murine IgG3 upper hinge region with additional residues"
FT	FT	Domain	/label= dHLX-dimerisation_domain

[illegible]

DE	23-MAY-2000	(first entry)
XX	M79scFv-interleukin 2-fusion protein containing tetramerisation domain.	
XX		
KW	Murine; M79 antibody; 17-1A antigen; single-chain Fv fragment; scFv;	
KW	fusion construct; human; interleukin 2; IL-2; tetramerisation domain;	
KW	heteromolecule; multifunctional compound; constant domain;	
KW	immunoglobulin; cytosolic; immunostimulatory; antileukemia; diagnosis;	
KW	antiproliferative; prevention; treatment; malignant; haematopoietic cell;	
KW	lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.	
XX		
OS	Chimeric - Mus sp.	
OS	Chimeric - Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	Peptide	1..19
FT		/label= Leader_peptide
FT	Region	20..126
FT		/label= M79scFv_light_chain_variable_region
FT	Region	127..141
FT		/label= Gly-Ser_Linker
FT	Region	142..256
FT		/label= M79scFv_heavy_chain_variable_region
FT	Region	259..269
FT		/note= "Human IgG3 upper hinge region with additional residues"
FT	Domain	270..308
FT		/label= Human_p53_tetramerisation_domain
FT	Peptide	309..315
FT		/label= Short_peptide_linker
FT	Domain	316..450
FT		/label= Interleukin-2_domain
FT	Region	451..456
FT		/label= His_tag
XX		
PN	WO200006605-A2.	
XX		
PD	10-FEB-2000.	
XX		
PF	28-JUL-1999;	99WO-EP05416.
XX		
PR	28-JUL-1998;	98EP-0114082.
XX		
PA	(M1CR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.	
XX		
PI	Kuifer P, Dreier T, Baeuerle PA, Borschert K, Zetl F;	
XX		
DR	WPI: 2000-195265/17.	
DR	N-PSDB: Z50585.	
XX		
PT	New multifunctional compounds useful for preventing and/or treating	
PT	malignant cell growth and for detection and diagnosis	
XX		
PS	Example 9; Fig 48; 166pp; English.	
XX		
CC	The patent discloses heteromolecules which are multifunctional compounds	
CC	producible in a mammalian host cell as a secretable and fully functional	
CC	heterodimer of two polypeptide chains, where one of the polypeptide	
CC	chains comprises, a CH1-domain (constant domain of an immunoglobulin	
CC	heavy chain) and the other chain comprises CL-domain (constant domain of	
CC	an immunoglobulin light chain). The polypeptide chains further comprise,	
CC	fused to the constant domains at least two (poly)peptides having	
CC	different receptor or ligand functions, where further at least two of the	
CC	different (poly)peptides lack an intrinsic affinity for one another and	
CC	are linked via the constant domains. The heteromolecules have	
CC	cytostatic, immunostimulatory, antileukemia and antiproliferative	
CC	activities. These compounds can be used for diagnosing, preventing and	
CC	treating malignant cell growth related to malignancies of hematopoietic	
CC	cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,	
CC	melanomas and sarcomas.	
CC	The present sequence is a fusion protein comprising murine	
CC	17-1A-antigen specific M79 single-chain Fv (scFv) fragment at the	
CC	N-terminus, human interleukin-2 at the C-terminus and a tetramerisation	

CC The present sequence is that of the light chain variable region
CC (VL) of 369, a murine monoclonal antibody (mAb) produced by hybridoma
CC cell line 369. mAb 369 competes with erythropoietin for binding to
CC the erythropoietin receptor (EpoR), and is characterised by agonist

CC Q94484 is the plasmid pUC-M21-V(L), which encodes R76663 the
CC murine antibody ONS-21 variable light chain. The plasmid was
CC used in the construction of an expression vector, contg. cDNA
CC encoding a human/murine chimeric antibody, reactive with

CC human medulloblastoma (a brain tumour) cells. The chimeric
CC antibody can be used in the diagnosis and treatment of this
CC disease.
XX
SQ Sequence 127 AA;

Query Match 89.9%; Score 517; DB 16; Length 127;
Best Local Similarity 92.5%; Pred. No. 5e-37; Mismatches 0; Gaps 0;
Matches 99; Conservative 1; Indels 7;

OY 4 DIOMIQSKFMSTSVGDRVTYTCRASNQVGNVAMVQOKPGOSPNNALITYSASYRSGVPD 63
||| |
Db 21 divmtqsgkfmsvsgdrvtvckasqngvgnvawygqkpgspkpllysasysrysgvpd 80
OY 64 RFTGSGSGTDFLTITTNQSEDLADYFCQOYNSTPLRTGTGKLEIK 110
|||||
Db 81 rftgsgsgtdfltltnvgsedladyfcqynsypratgggtkleik 127

RESULT 5
W04378
ID W04378 standard; Protein; 127 AA.

AC W04378;
XX
DT 04-DEC-1996 (first entry)

XX Chimeric human/murine MAb ONS-M21 variable light region.

XX Light: variable region; murine; human; myeloblastoma; chimera;
KW monoclonal antibody; chimera; single stranded Fv region;
KW low human antigenicity; diagnosis; treatment; cerebral tumour;
KW reshaped.

XX Synthetic.

OS
FH Key Location/Qualifiers
FT Peptide 1..24
FT /label- sig-peptide
FT 25..127
FT /label- mat-peptide
FT 48..58
FT /label- CDR_1
FT 74..80
FT /label- CDR_2
FT 113..121
FT Region /label- CDR_3

XX JP08169900-A.

XX 02-JUL-1996.

XX 18-NOV-1994; 94JP-0285057.

XX 18-OCT-1994; 94JP-0252166.

XX 19-NOV-1993; 93JP-0291078.

XX (CHUS) CHUGAI PHARM CO LTD.

XX WPI: 1996-358509/36..

XX N-PSDB: T38599.

XX Reshaped anti-human myeloblastoma cell human antibody - has low
XX human antigenicity, and is therefore useful for diagnosis and
XX treatment of cerebral tumours, e.g. myeloblastoma

XX Example 2; Pages 21-22; 45pp; Japanese.

XX The present sequence is the variable light region of the
CC chimeric human/murine monoclonal antibody (Mab) ONS-M21. The Mab
CC was prepd. by combining light and heavy variable region DNA,
CC from a murine anti-human myeloblastoma cell Mab, with human light
CC

CC and heavy constant region sequences, respectively to produce
CC chimeric human/murine light and heavy chain DNA mols.. A
CC recombinant vector for the expression of the heavy and light chain
CC DNA mols. was prepd., and used to transform a host cell. The host
CC cell was then cultured, and the expression prods. of the heavy and
CC light chain DNA mols. sepd. and connected with a peptide linker to
CC produce a single stranded Fv region. The reshaped Fv region has
CC low human antigenicity, and is therefore expected to be useful as
CC an agent for the diagnosis and treatment of cerebral tumours,
e.g. myeloblastoma.

SQ Sequence 127 AA;

Query Match 89.9%; Score 517; DB 17; Length 127;
Best Local Similarity 92.5%; Pred. No. 5e-37; Mismatches 0; Gaps 0;
Matches 99; Conservative 1; Indels 7;

OY 4 DIOMIQSKFMSTSVGDRVTYTCRASNQVGNVAMVQOKPGOSPNNALITYSASYRSGVPD 63
||| |
Db 21 divmtqsgkfmsvsgdrvtvckasqngvgnvawygqkpgspkpllysasysrysgvpd 80
OY 64 RFTGSGSGTDFLTITTNQSEDLADYFCQOYNSTPLRTGTGKLEIK 110
|||||
Db 81 rftgsgsgtdfltltnvgsedladyfcqynsypratgggtkleik 127

RESULT 6

W01591
ID W01591 standard; Protein; 107 AA.

AC W01591;

XX 22-AUG-1997 (first entry)

XX Lead binding Mab 2E7 light chain variable region.

XX Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
KW pharmaceutical; health care; skin treatment; pesticide; herbicide;
KW heavy metal.

XX Mus musculus.

XX W09639518-A1.

XX 12-DEC-1996.

XX 05-JUN-1996; 96WO-US09258.

XX 10-OCT-1995; 95US-0541373.

XX 05-JUN-1995; 95US-0462798.

XX (BION-) BIONEERASKA INC.

XX Lopez O, Murray PJ, Wylie DE;

XX WPI: 1997-043140/04.

XX N-PSDB: T58265.

XX DNA encoding heavy metal binding polypeptide sequences - used for
XX detecting, removing, adding or neutralising heavy metals, such as
XX lead cations

XX Claim 19; Page 85; 125pp; English.

XX The present sequence represents the light chain variable region for
CC monoclonal antibody (Mab) 2E7, which immunoreacts with a lead cation.
CC The sequence was derived from RNA isolated from mouse hybridoma cells.
CC The protein can be used for binding heavy metals, such as lead cations.
CC It can be used for detecting, removing, adding or neutralising the
CC heavy metals in biological and inanimate systems. It can be used in
CC e.g. aqueous liquid systems, in biological or environmental systems or
CC in such compositions as perfumes, cosmetics, pharmaceuticals, health


```

FT Region 90..98 "complementarity determining region (CDR) as
FT /note= indicated by Kabat sequence comparison"
FT Region 92..98
FT /note= "complementarity determining region (CDR) as
FT indicated by X-ray crystallography"
XX PN US568670-A.
XX PD 11-NOV-1997.
XX PF 01-MAR-1995; 95US-0398612.
XX PR 01-MAR-1995; 95US-0398612.
XX PR 03-MAR-1994; 94US-0205864.
XX PA (GETH ) GENENTECH INC.
XX PA (INDV ) UNIV INDIANA.
XX PI Doerschuk CM, Fong S, Hebert CA, Kim KJ, Leong SR;
DR WPI: 1997-558085/51.
DR N-PDB: V03200.
XX PT Treatment of bacterial pneumonia - with monoclonal antibody specific
PT for interleukin-8; inhibits lung inflammatory conditions
XX PS Claim 5; Fig 16; 63pp; English.
XX CC The present sequence represents the light chain variable region of the
CC monoclonal antibody 5.12.14. This antibody is a murine anti
CC interleukin-8 (IL-8) IgG2a isotype. IL-8 is a neutrophil
CC chemotactic peptide secreted by a variety of cells in response to
CC inflammatory mediators. IL-8 can play an important role in the
CC pathogenesis of inflammatory disorders such as adult respiratory
CC distress syndrome (ARDS), septic shock and multiple organ failure.
CC Treatment of bacterial pneumonia in a mammal comprises administering an
CC anti IL-8 monoclonal antibody, such as 5.12.14, that binds human IL-8
CC with a Kd of 10-8 to 10-11 M, inhibits neutrophil chemotaxis in
CC response to IL-8, inhibits IL-8 mediated elastase release by
CC neutrophils and does not bind to C5a, beta-TG or platelet factor 4.
CC IL-8 specific monoclonal antibodies are especially for treating
CC pneumonia caused by Streptococcus pneumoniae, E. coli or Pseudomonas
CC aeruginosa in humans. The antibodies may also be used in the treatment
CC of ulcerative colitis and other inflammatory conditions.
XX SQ Sequence 123 AA;
SQ
Query Match 89.4%; Score 514; DB 18; Length 123;
Best Local Similarity 90.7%; Pred. No. 8.7e-37;
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0.
OY 4 DIOMOSQKPFMTSTVGDRVTVCRAKSONGVNAVWVVOOKPQGSPNALITYSASRYSGVPD 63
Db 1 diwmqsqklnstsvsgdvtsvvtckssqngrlvavayqqgpgpspxallyssysrysgvpd 60
OY 64 RFTGSGSGTDFLTITTNVQSEDLADYFCQOVNSYPFLTEGTGRKLEIK 110
Db 61 rftgsgsgtfdltitshvgsedladycfqgnylplttfpgpykgleik 107
RESULT 9
W31574
W31574 standard; Protein: 123 AA.
AC W31574;
XX 24-FEB-1998 (first entry)
XX Anti IL-8 monoclonal antibody (5.12.14) light chain variable region.
XX murine light chain; 5.12.14; human interleukin-8; IL-8; anti IL-8;

```

XX	Mus sp.		
XX	Key	Location/Qualifiers	
FH	Region	1..109	"light chain variable region"
FT		/note=	
FT	Region	24..34	"complementarity determining region 1; determined by Kabat sequence comparison"
FT		/note=	
FT	Region	26..32	"complementarity determining region 1; determined by X-ray crystallography"
FT		/note=	
FT	Region	50..56	"complementarity determining region 2; determined by Kabat sequence comparison"
FT		/note=	
FT	Region	50..52	"complementarity determining region 2; determined by X-ray crystallography"
FT		/note=	
FT	Region	89..97	"complementarity determining region 3; determined by Kabat sequence comparison"
FT		/note=	
FT	Region	91..97	"complementarity determining region 3; determined by X-ray crystallography"
FT		/note=	
FT	Region	110..123	"partial constant light region"
XX			
PN	US5677426-A.		
PD	14-OCT-1997.		
XX			
PF	01-MAR-1995;	95US-0398613.	
PR	01-MAR-1995;	95US-0398613.	
PR	03-MAR-1994;	94US-0205864.	
XX			
PA	(GETH) GENENTECH INC.		
PI	Fong S, Hebert CA, Kim KJ, Leong SR;		
DR	WPI; 1997-511926/47.		
XX	N-PSTDB; T93543.		
PT			
PT	Fragments of antibody to human interleukin-8 - comprising light and/or heavy chain sequences; used to prevent interleukin-8 mediated neutrophil chemotaxis		
XX			
PS	Disclosure; Fig 16; 63pp; English.		
CC			
CC	This is the light chain variable region and a partial constant region of the murine monoclonal antibody 5.12.14. The variable region comprises of complementarity determining regions (CDR). The encoding cDNA was cloned into vector pBl3.1 to construct pAS1214VL which was used in the construction of a chimeric 5.12.14 Fab vector by various recombinant techniques. This chimeric Fab comprises of CDRs of a light chain and/or a heavy chain variable region from the murine species and light chain and/or heavy chain constant region of the human immunoglobulin IgG1.		
CC	This recombinant human-murine chimeric Fab has anti interleukin-8 (IL-8) activity and can inhibit the IL-8 binding to human neutrophils. This anti IL-8 Fab is used to prevent interleukin-8 mediated neutrophil chemotaxis which is useful in the treatment of ulcerative colitis and bacterial pneumonia.		
XX			
SQ	Sequence 123 AA:		
Query Match	89.4%; Score 514; DB 18; Length 123;		
Best Local Similarity	90.7%; Pred. NO. 8.7e-37;		
Matches 97; Conservative	5; Indels 0; Gaps 0		

CC	antibody Anti-IL-8 antibodies are especially used to treat or prevent
CC	allergic asthma in humans. They inhibit: (a) neutrophil chemotaxis in
CC	response to IL-8; (b) IL-8-mediated release of elastase from neutrophils
CC	and (c) binding of IL-8 to neutrophils. Anti-IL-8 antibodies can be used
CC	to treat many other inflammatory disorders, e.g. ischemic reperfusion,
AR	ARDS, dermatitis, particularly bacterial pneumonia and inflammatory
CC	bowel disease.
XX	
XX	Sequence 123 AA:
OY	Query Match 89.4% Score 514; DB 18; Length 123; Best Local Similarity 90.7%; Pred. No. 8.7e-37;
Db	Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
OY	4 DDIQIOSKFMSTVSGDVFVTCKRASNQWNTNVMYQQKPGCSNALIYSASRYSGVPD 63 Db 1 dvmtgsgqkfmstvsygdvsvtlckasqngvgnwagygqkpggsphallyssasyrsgvpd 60
OY	64 RFTGSGCTDETLTITNQSEDLADYFCQOYNISYPLRTGTKEIK 110 Db 61 rftgsgydlflltshvgsedladyfcqgyinyplrtgpptkleik 107
RESULT	11
ID	W69305 standard; Protein; 123 AA.
XX	W69305;
AC	
XX	W69305;
DT	15-FEB-1999 (first entry)
XX	
DE	Murine anti-IL-8 Mab 5.12.14 light chain.
XX	
KM	Humanized antibody; monoclonal antibody; mouse; interleukin-8;
KM	inflammation; immunotherapy; therapy; psoriasis;
KM	inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KM	ischemic reperfusion; adult respiratory distress syndrome;
KM	dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;
KM	rheumatoid arthritis; Sjorgen's syndrome; vasculitis;
KM	leukocyte diapedesis; multiple organ injury syndrome; septicemia;
KM	trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis;
KM	vasculitis; bronchitis; bronchiectasis; cystic fibrosis; diagnosis.
XX	
OS	Mus sp.
XX	
FH	Location/Qualifiers
FT	1..109 /note= "light chain variable region"
FT	110..123 /note= "constant region"
FT	Region
FT	24..34 /label= CDR1
FT	/note= "complementarity determining region
FT	determined by Kabat sequence comparison"
FT	Region
FT	26..32 /label= CDR1
FT	/note= "complementarity determining region
FT	determined by X-ray crystallography"
FT	Region
FT	50..56 /label= CDR2
FT	/note= "complementarity determining region
FT	determined by Kabat sequence comparison"
FT	Region
FT	50..52 /label= CDR2
FT	/note= "complementarity determining region
FT	determined by X-ray crystallography"xx
FT	Region
FT	89..97 /label= CDR3
FT	/note= "complementarity determining region
FT	determined by Kabat sequence comparison"
FT	Region
FT	91..97 /label= CDR3
FT	

CC reperfusion disorder, and autoimmune diseases. They can also be used
CC for treating e.g. inflammatory skin diseases including psoriasis and
CC atopic dermatitis, systemic scleroderma and sclerosis, and asthmatic
CC diseases. The conjugates can also be used as reagents in an animal
CC model system for in vivo study of the biological functions of the
CC antigen recognised by the conjugate. The present sequence represents
CC a fragment of the murine 5.12.14 anti-IL-8 monoclonal antibody,
CC which is used in an example from the present invention.
XX
SQ Sequence 123 AA:

Query Match 89.4%; Score 514; DB 20; Length 123;
Best Local Similarity 90.7%; Pred. No. 8.7e-37;
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 4 DIOMIQSQRKFMSTSVGDRVVTCTKASQNVGTNNAMWYQKRGQSPNALIYSASTRYSGVPD 63
DB 1 dlymtgqkfstsvgdvsvtckasqnyglvawyqkpgqspkallyssyrysgvpd 60
QY 64 RFTGSGSGTDFTLTITNWQSEDLADYFCQOYNSYPLTFGTGKLEIK 110
DB 61 rftgsgsgtdftltitlnwqsedladyfcqgynilypltfpgptkleik 107

RESULT 15

B30299
ID B30299 standard; Protein; 123 AA.

AC B30299;

DT 12-FEB-2001 (first entry)

DE Murine anti-IL-8 antibody light chain SEQ ID NO: 17.

KM Humanised antibody; anti-IL-8; interleukin-8; inflammation; septic shock;
KW adult respiratory distress syndrome; multiple organ failure;
KW bacterial pneumonia; inflammatory bowel disease.

XX
OS Mus sp.

PN US6133426-A.

PD 17-OCT-2000.

PF 20-FEB-1998; 98US-0026985.

PR 21-FEB-1997; 97US-0038664.

PR 22-JAN-1998; 98US-0074330.

PA (GETH) GENENTECH INC.

PI Presta LG, Leong SR, Gonzalez TN;

DR WPI; 2000-686027/67.

PT Humanized anti-interleukin 8 monoclonal antibody variant useful for
PT treating inflammatory disorders, such as adult respiratory distress
PT syndrome, hypovolemic shock and ulcerative colitis -

PS Example C; Column 139-140; 240pp; English.

CC The present invention provides a number of humanised monoclonal anti-IL-8
CC antibodies which can be used in the diagnosis and treatment of
CC inflammatory disorders, including adult respiratory distress syndrome,
CC septic shock, multiple organ failure, bacterial pneumonia and
CC inflammatory bowel disease. The present sequence comprises one of the
CC antibodies of the invention.
XX
SQ Sequence 123 AA:

Query Match 89.4%; Score 514; DB 21; Length 123;

Best Local Similarity 90.7%; Pred. No. 8.7e-37;
Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 4 DIOMIQSQRKFMSTSVGDRVVTCTKASQNVGTNNAMWYQKRGQSPNALIYSASTRYSGVPD 63
DB 1 dlymtgqkfstsvgdvsvtckasqnyglvawyqkpgqspkallyssyrysgvpd 60

QY 64 RFTGSGSGTDFTLTITNWQSEDLADYFCQOYNSYPLTFGTGKLEIK 110
DB 61 rftgsgsgtdftltitlnwqsedladyfcqgynilypltfpgptkleik 107

Search completed: June 20, 2001, 11:15:24
Job time: 1665 sec